

Thu Dec 15 12:21:43 2005

us-10-063-557-50.multi.rag

Blanchard, D.
10/06/3557 Page 1
Seq ID 50

GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: December 14, 2005, 06:19:30 ; Search time 121 Seconds
(without alignments)
323.179 Million cell updates/sec

Title: US-10-063-557-50

Perfect score: 461

Sequence: 1 MERTVALLLLAGLTALBAN.....HSPVEKALPITPGSATTC 89
BLOSUN62

Scoring table:

Gapop 10.0, Gapext 0.5
2443163 seqs, 439378781 residues

Searched: 2443163
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 1500 summaries

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description

RESULT 1
ID AAY66705 standard; protein; 89 AA.
DE Membrane-bound protein PRO1069.
PN WO9563088-A2.
PD 09-DEC-1999.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 2
ID AAY67258 standard; protein; 89 AA.
DE Human signal peptide containing protein HSP-35 SEQ ID NO:35.
PN WO20000610-A2.
PD 06-JAN-2000.

PA (INCY-) INCYTE PHARM INC.
Query Match 100.0%; Score 461; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 3
ID AAY65679 standard; protein; 89 AA.
DE Human kidney disease associated protein SEQ ID 11.
PN WO200061622-A2.
PD 19-OCT-2000.

PA (INCY-) INCYTE PHARM INC.
Query Match 100.0%; Score 461; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 4
ID AAU29123 standard; protein; 89 AA.
DE Human PRO polypeptide sequence #100.
PN WO200168848-A2.
PD 20-SEP-2001.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 5
ID AAB87550 standard; protein; 89 AA.
DE Human PRO1069.
PN WO200116318-A2.
PD 08-MAR-2001.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

DE Human PRO1069 (UNQ526) protein sequence SEQ ID NO:262.
PN WO200073454-A1.
PD 07-DEC-2000.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 7
ID ABG5875 standard; protein; 89 AA.
DE Human secreted/transmembrane protein PRO1069.
PN US200219130-A1.
PD 29-AUG-2002.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 8
ID ABUS8499 standard; protein; 89 AA.
DE Human PRO polypeptide #100.
PN US200302727-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 9
ID ABUS8047 standard; protein; 89 AA.
DE Novel human secreted and transmembrane protein PRO1069.
PN US2003032127-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 10
ID ABUS4362 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003032112-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 11
ID ABR66236 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003027278-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 12
ID ABR65626 standard; protein; 89 AA.
DE Human secreted polypeptide PRO1069, SEQ ID NO:200.
PN US2003036159-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 13
ID ABUS9566 standard; protein; 89 AA.
DE Human secreted/transmembrane protein (PRO) #100.
PN US2003040070-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

RESULT 14
ID ABUS8043 standard; protein; 89 AA.
DE Human PRO polypeptide #75.
PN US2003027163-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 461; DB 6; Length 89;
Best Local Similarity 100.0%; Pred. No. 4e-50;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 06:27:56 ; Search time 33 Seconds

(without alignments)
222.974 Million cell updates/sec

Perfect score: 461
Sequence: 1 MERVTLALLAGLTALEAN.....HSPVPEKAIPLITPGSARTTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCrus-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	89	2	US-09-289-349-11
6	276.5	60.0	88	2	US-09-724-864-58
7	256.5	55.6	87	1	US-08-725-531-5
8	256.5	55.6	87	1	US-08-738-127-5
9	256.5	55.6	87	1	US-09-213-392-5
10	256.5	55.6	87	1	US-09-083-661-5
11	214.5	46.5	87	1	US-08-289-247B-4
12	214.5	46.5	87	1	US-08-725-531-4
13	214.5	46.5	87	1	US-08-738-127-4
14	214.5	46.5	87	1	US-09-213-392-4
15	214.5	46.5	87	1	US-09-083-661-4
16	214.5	46.5	124	2	US-09-949-016-8238
17	214.5	46.5	124	2	US-09-949-016-8239
18	191.5	41.5	178	2	US-09-949-016-9028
19	191.5	41.5	178	2	US-09-949-016-9029
20	131	28.4	106	2	US-09-621-976-5338
21	131	28.4	107	2	US-09-621-976-5332
22	129	28.0	92	1	US-08-738-127-1
23	129	28.0	92	1	US-09-247-135-120
24	129	28.0	92	2	US-09-148-545-238
25	129	28.0	92	2	US-09-621-011-238
26	129	28.0	92	2	US-09-903-190-120
27	129	28.0	93	2	US-09-148-545-183
28	129	28.0	93	2	US-09-621-011-183
29	126.5	27.4	92	1	US-08-725-531-3
30	126.5	27.4	92	1	US-08-738-127-3
31	126.5	27.4	92	1	US-09-213-392-3
32	126.5	27.4	92	1	US-09-083-661-3

33	121	26.2	70	2	US-09-148-545-269	Sequence 269, App
34	121	26.2	70	2	US-09-621-011-269	Sequence 269, App
35	112.5	24.4	95	1	US-08-725-531-1	Sequence 1, Appl
36	112.5	24.4	95	1	US-09-213-392-1	Sequence 1, Appl
37	112.5	24.4	95	1	US-09-083-661-1	Sequence 1, Appl
38	112.5	24.4	96	2	US-09-149-476-473	Sequence 473, App
43	106	23.0	69	2	US-09-149-476-606	Sequence 606, App
44	103.5	22.5	95	2	US-09-621-976-5250	Sequence 5250, App
45	99.5	21.6	72	2	US-08-905-223-405	Sequence 405, App
46	94	20.4	179	2	US-09-205-258-424	Sequence 424, App
47	94	20.4	179	2	US-10-004-860-424	Sequence 424, App
48	89	19.3	80	2	US-09-621-976-6085	Sequence 6085, App
49	83	18.0	86	2	US-09-949-016-8419	Sequence 8419, App
50	83	18.0	86	2	US-09-949-016-8420	Sequence 8420, App
51	73.5	15.9	58	1	US-08-725-531-6	Sequence 6, Appl
52	73.5	15.9	58	1	US-08-738-127-6	Sequence 6, Appl
53	73.5	15.9	58	1	US-09-213-392-6	Sequence 6, Appl
54	73.5	15.9	58	1	US-09-083-661-6	Sequence 6, Appl
55	67.5	14.6	664	2	US-09-268-140-2	Sequence 2, Appl
56	67.5	14.6	664	2	US-09-949-016-9005	Sequence 9005, App
57	66.5	14.4	376	2	US-09-198-452A-1112	Sequence 1112, App
58	66.5	14.4	388	2	US-09-438-185A-1038	Sequence 1038, App
59	66.5	14.4	523	2	US-09-949-016-6195	Sequence 6195, App
60	66.5	14.4	552	2	US-09-949-016-8164	Sequence 8164, App
61	64.5	14.0	729	2	US-09-248-796A-17121	Sequence 17121, A
62	63	13.7	627	2	US-10-223-100-3	Sequence 3, Appl
63	62.5	13.6	339	2	US-09-690-454-66	Sequence 66, Appl
64	62.5	13.6	340	2	US-09-690-454-174	Sequence 174, App
65	62.5	13.6	389	2	US-09-328-352-7324	Sequence 7324, App
66	62	13.4	78	2	US-09-749-637A-342	Sequence 342, App
67	62	13.4	360	2	US-09-489-039A-8000	Sequence 8000, App
68	62	13.4	601	2	US-09-336-649A-4	Sequence 4, Appl
69	61.5	13.3	103	2	US-09-107-532A-3725	Sequence 3725, App
70	61.5	13.3	433	2	US-09-198-452A-825	Sequence 925, App
71	61.5	13.3	453	2	US-09-438-185A-860	Sequence 860, App
72	61.5	13.3	549	2	US-09-120-365-3	Sequence 3, Appl
73	61.5	13.3	549	2	US-09-515-039-3	Sequence 3, Appl
74	61.5	13.3	606	2	US-09-270-767-41830	Sequence 41830, A
75	61.5	13.3	990	2	US-10-363-937-7	Sequence 7, Appl
76	61	13.2	457	2	US-09-489-039A-12762	Sequence 12762, A
77	60.5	13.1	106	2	US-09-149-476-341	Sequence 341, App
78	60.5	13.1	288	2	US-09-386-642-13	Sequence 13, Appl
79	60.5	13.1	998	2	US-09-252-991A-28424	Sequence 28424, A
80	60	13.0	234	2	US-09-248-796A-17625	Sequence 17625, A
81	60	13.0	337	2	US-08-930-830B-2	Sequence 2, Appl
82	60	13.0	342	2	US-08-930-830B-5	Sequence 5, Appl
83	60	13.0	404	2	US-09-949-016-7352	Sequence 7352, App
84	60	13.0	426	2	US-09-252-991A-27522	Sequence 27522, A
85	60	13.0	497	2	US-09-718-693A-1	Sequence 1, Appl
86	59	12.8	83	2	US-09-227-357-652	Sequence 652, App
87	59	12.8	83	2	US-09-973-278-370	Sequence 370, App
88	59	12.8	430	2	US-09-134-000C-4819	Sequence 4819, App
89	59	12.8	539	1	US-08-464-340A-13	Sequence 13, Appl
90	59	12.8	806	2	US-09-833-466-13	Sequence 13, Appl
91	59	12.8	854	2	US-09-833-466-12	Sequence 12, Appl
92	59	12.8	858	2	US-09-275-252A-6	Sequence 6, Appl
93	58.5	12.7	142	2	US-09-543-681A-5222	Sequence 5222, App
94	58.5	12.7	200	2	US-09-252-991A-27855	Sequence 27855, A
95	58.5	12.7	243	2	US-09-107-533A-9908	Sequence 4908, App
96	58.5	12.7	260	2	US-09-070-526-2	Sequence 2, Appl
97	58.5	12.7	260	2	US-09-618-259-7	Sequence 7, Appl
98	58.5	12.7	383	1	US-08-314-596-41	Sequence 41, Appl
99	58.5	12.7	383	1	US-08-320-982-41	Sequence 41, Appl
100	58.5	12.7	383	1	US-08-819-037-41	Sequence 41, Appl
101	58.5	12.7	383	2	US-08-530-862B-6	Sequence 6, Appl
102	58.5	12.7	383	2	US-08-597-311D-6	Sequence 6, Appl
103	58.5	12.7	383	2	US-09-059-769-9	Sequence 9, Appl
104	58.5	12.7	383	2	US-09-161-994A-14	Sequence 14, Appl
105	58.5	12.7	383	2	US-09-133-962A-2	Sequence 2, Appl
106	58.5	12.7	383	2	US-09-045-940-41	Sequence 41, Appl
107	58.5	12.7	383	2	US-09-763-331-4	Sequence 4, Appl
108	58.5	12.7	383	2	US-09-697-379-2	Sequence 2, Appl
109	58.5	12.7	383	2	US-10-116-212A-2	Sequence 2, Appl
110	58.5	12.7	383	2		
111	58.5	12.7	383	2		

112	58.5	12.7	383	2	US-09-885-189-6	Sequence 6, Appli	185	56	12.1	605	2	US-09-252-991A-24349	Sequence 24349, A
113	58.5	12.7	1058	2	US-09-902-540-1949	Sequence 14949, A	186	56	12.1	1058	2	US-09-949-016-11457	Sequence 11457, A
114	58.5	12.7	1518	2	US-09-489-039A-11177	Sequence 11177, A	187	56	12.1	1384	2	US-08-826-134-2	Sequence 2, Appli
115	58	12.6	428	2	US-09-489-039A-10271	Sequence 10271, A	188	56	12.1	1384	2	US-09-949-016-6395	Sequence 6395, Ap
116	58	12.6	427	2	US-09-902-540-14326	Sequence 14326, A	189	56	12.1	1633	2	US-09-902-540-12892	Sequence 12892, A
117	58	12.6	681	2	US-10-104-047-3586	Sequence 3586, Ap	190	56	12.1	1805	2	US-09-949-016-8246	Sequence 8246, Ap
118	57.5	12.5	27	2	US-09-962-756-1544	Sequence 1644, Ap	191	55.5	12.0	175	2	US-09-252-991A-32945	Sequence 32945, A
119	57.5	12.5	352	2	US-09-252-991A-17455	Sequence 17455, A	192	55.5	12.0	248	1	US-08-313-553-3	Sequence 3, Appli
120	57.5	12.5	471	2	US-09-252-991A-77897	Sequence 77897, A	193	55.5	12.0	248	1	US-08-303-651-2	Sequence 2, Appli
121	57.5	12.5	471	2	US-09-328-352-5145	Sequence 5145, Ap	194	55.5	12.0	248	2	US-08-767-993-3	Sequence 3, Appli
122	57.5	12.5	499	2	US-09-902-540-12205	Sequence 12205, A	195	55.5	12.0	262	1	US-08-313-553-2	Sequence 2, Appli
123	57.5	12.5	528	1	US-08-527-152-2	Sequence 12305, A	196	55.5	12.0	262	2	US-08-767-993-2	Sequence 2, Appli
124	57.5	12.5	775	2	US-09-252-991A-28461	Sequence 28461, A	197	55.5	12.0	292	1	US-08-555-568B-19	Sequence 19, Appli
125	57.5	12.5	1107	2	US-09-489-039A-8890	Sequence 8890, Ap	198	55.5	12.0	292	2	US-09-519-223-19	Sequence 19, Appli
126	57	12.4	185	2	US-10-018-924-6	Sequence 6, Appli	199	55.5	12.0	292	2	US-09-927-180-19	Sequence 19, Appli
127	57	12.4	647	2	US-09-543-681A-5240	Sequence 5240, Ap	200	55.5	12.0	348	2	US-09-248-796A-19460	Sequence 19460, A
128	56.5	12.3	89	1	US-07-939-501A-2	Sequence 2, Appli	201	55.5	12.0	384	1	US-08-675-650B-2	Sequence 2, Appli
129	56.5	12.3	89	1	US-07-966-187-5	Sequence 5, Appli	202	55.5	12.0	384	2	US-09-354-221B-14	Sequence 14, Appli
130	56.5	12.3	89	1	US-08-371-121-4	Sequence 4, Appli	203	55.5	12.0	384	2	US-09-354-221B-16	Sequence 16, Appli
131	56.5	12.3	89	2	US-07-927-391-6	Sequence 6, Appli	204	55.5	12.0	384	2	US-09-354-221B-18	Sequence 18, Appli
132	56.5	12.3	89	2	US-08-115-753-15	Sequence 15, Appli	205	55.5	12.0	384	2	US-09-128-602B-14	Sequence 16, Appli
133	56.5	12.3	158	2	US-09-107-532A-6092	Sequence 6092, Ap	206	55.5	12.0	384	2	US-09-128-602B-16	Sequence 18, Appli
134	56.5	12.3	168	2	US-09-898-659-16	Sequence 16, Appli	207	55.5	12.0	384	2	US-09-128-602B-18	Sequence 18, Appli
135	56.5	12.3	205	2	US-08-818-112-80	Sequence 80, Appli	208	55.5	12.0	384	2	US-09-995-287-14	Sequence 14, Appli
136	56.5	12.3	205	2	US-08-818-111-81	Sequence 80, Appli	209	55.5	12.0	384	2	US-09-995-287-16	Sequence 16, Appli
137	56.5	12.3	205	2	US-09-056-556-80	Sequence 81, Appli	210	55.5	12.0	384	2	US-09-995-287-18	Sequence 18, Appli
138	56.5	12.3	205	2	US-09-072-596-81	Sequence 81, Appli	211	55.5	12.0	391	2	US-09-489-039A-9791	Sequence 9791, Ap
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140	56.5	12.3	205	2	US-10-193-002-81	Sequence 81, Appli	213	55.5	12.0	459	1	US-08-313-553-15	Sequence 15, Appli
141	56.5	12.3	205	2	US-10-084-884-80	Sequence 80, Appli	214	55.5	12.0	559	2	US-08-767-993-15	Sequence 15, Appli
142	56.5	12.3	213	2	US-09-605-703B-2594	Sequence 2594, Ap	215	55.5	12.0	687	1	US-08-555-568B-21	Sequence 21, Appli
143	56.5	12.3	213	2	US-08-818-112-76	Sequence 76, Appli	216	55.5	12.0	687	2	US-09-519-223-21	Sequence 21, Appli
144	56.5	12.3	233	2	US-08-818-111-77	Sequence 76, Appli	217	55.5	12.0	687	2	US-09-927-180-21	Sequence 21, Appli
145	56.5	12.3	233	2	US-09-056-556-76	Sequence 76, Appli	218	55.5	12.0	688	1	US-08-555-568B-23	Sequence 23, Appli
146	56.5	12.3	233	2	US-09-072-596-77	Sequence 76, Appli	219	55.5	12.0	688	2	US-09-519-223-23	Sequence 23, Appli
147	56.5	12.3	233	2	US-09-072-967-76	Sequence 76, Appli	220	55.5	12.0	688	2	US-09-927-180-23	Sequence 23, Appli
148	56.5	12.3	233	2	US-10-193-002-77	Sequence 77, Appli	221	55.5	12.0	819	2	US-09-949-016-10948	Sequence 10948, A
149	56.5	12.3	233	2	US-10-084-843-76	Sequence 76, Appli	222	55.5	12.0	887	2	US-09-077-940A-2	Sequence 2, Appli
150	56.5	12.3	260	2	US-09-008-271A-7	Sequence 7, Appli	223	55.5	12.0	888	2	US-09-077-940A-4	Sequence 4, Appli
151	56.5	12.3	260	2	US-09-968-415-7	Sequence 7, Appli	224	55.5	12.0	968	2	US-09-228-986-76	Sequence 76, Appli
152	56.5	12.3	385	1	US-08-416-756A-3	Sequence 3, Appli	225	55.5	12.0	968	2	US-10-101-464A-76	Sequence 76, Appli
153	56.5	12.3	385	2	US-08-880-865-3	Sequence 3, Appli	226	55	11.9	124	2	US-09-270-767-33906	Sequence 33906, A
154	56.5	12.3	419	2	US-08-115-753-2	Sequence 2, Appli	227	55	11.9	124	2	US-09-270-767-49123	Sequence 49123, A
155	56.5	12.3	419	2	US-08-115-753-33	Sequence 33, Appli	228	55	11.9	205	2	US-09-248-796A-15224	Sequence 15224, A
156	56.5	12.3	601	2	US-09-949-016-9977	Sequence 9977, Ap	229	55	11.9	232	1	US-08-456-670B-39	Sequence 39, Appli
157	56.5	12.3	626	2	US-09-957-187-83	Sequence 83, Appli	230	55	11.9	232	1	US-09-372-036-39	Sequence 39, Appli
158	56.5	12.3	630	2	US-09-520-781-30	Sequence 30, Appli	231	55	11.9	359	2	US-09-248-796A-18202	Sequence 18202, A
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160	56.5	12.3	630	2	US-09-991-053-30	Sequence 30, Appli	233	55	11.9	376	2	US-09-631-584-51	Sequence 51, Appli
161	56.5	12.3	697	2	US-10-101-464A-940	Sequence 940, App	234	55	11.9	381	2	US-09-248-796A-19630	Sequence 19630, A
162	56.5	12.3	757	2	US-09-949-016-7121	Sequence 7121, Ap	235	55	11.9	404	2	US-09-538-092-50	Sequence 50, Appli
163	56.5	12.3	852	1	US-08-190-802A-59	Sequence 59, Appli	236	55	11.9	406	2	US-09-252-991A-20630	Sequence 20630, A
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165	56.5	12.3	852	2	US-08-477-346-59	Sequence 59, Appli	238	55	11.9	478	1	US-08-456-670B-40	Sequence 40, Appli
166	56.5	12.3	852	2	US-08-477-346-67	Sequence 67, Appli	239	55	11.9	478	2	US-09-372-036-40	Sequence 40, Appli
167	56.5	12.3	852	2	US-08-473-089-59	Sequence 59, Appli	240	55	11.9	484	1	US-08-117-499A-26	Sequence 26, Appli
168	56.5	12.3	852	2	US-08-473-089-67	Sequence 67, Appli	241	55	11.9	484	1	US-08-482-847-26	Sequence 26, Appli
169	56.5	12.3	852	2	US-08-487-072A-59	Sequence 59, Appli	242	55	11.9	512	1	US-08-173-508-4	Sequence 4, Appli
170	56.5	12.3	884	2	US-08-487-072A-67	Sequence 67, Appli	243	55	11.9	512	1	US-08-265-310-4	Sequence 4, Appli
171	56.5	12.3	884	2	US-09-520-781-6	Sequence 6, Appli	244	55	11.9	512	1	US-08-951-742-4	Sequence 4, Appli
172	56.5	12.3	884	2	US-09-957-187-6	Sequence 6, Appli	245	55	11.9	533	2	US-09-549-519-32	Sequence 32, Appli
173	56.5	12.3	884	2	US-09-991-053-6	Sequence 6, Appli	246	55	11.9	598	2	US-09-252-991A-25875	Sequence 25875, A
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175	56.5	12.3	939	2	US-09-957-187-4	Sequence 4, Appli	248	55	11.9	666	1	US-08-346-128-16	Sequence 16, Appli
176	56.5	12.3	939	2	US-09-991-053-4	Sequence 4, Appli	249	55	11.9	666	2	US-08-532-384-17	Sequence 37, Appli
177	56.5	12.3	1030	2	US-09-856-681A-2	Sequence 2, Appli	250	55	11.9	1481	1	US-08-616-844-40	Sequence 40, Appli
178	56.5	12.3	1030	2	US-09-856-681A-7	Sequence 7, Appli	251	55	11.9	1481	1	US-08-599-684-40	Sequence 40, Appli
179	56.5	12.3	1047	2	US-09-957-187-85	Sequence 85, Appli	252	55	11.9	1481	1	US-08-944-868A-40	Sequence 40, Appli
180	56	12.1	199	2	US-09-543-681A-5720	Sequence 5720, Ap	253	55	11.9	1481	2	US-08-944-433A-40	Sequence 40, Appli
181	56	12.1	202	2	US-09-489-039A-8619	Sequence 8619, Ap	254	55	11.9	1481	2	US-08-944-433A-40	Sequence 40, Appli
182	56	12.1	316	2	US-09-540-236-3467	Sequence 3467, Ap	255	54.5	11.8	102	2	US-09-540-236-2816	Sequence 2816, Ap
183	56	12.1	579	2	US-09-540-236-2071	Sequence 2071, Ap	256	54.5	11.8	139	2	US-09-270-767-2364	Sequence 2364, Ap
184	56	12.1	593	2	US-09-949-016-10355	Sequence 10355, A	257	54.5	11.8	139	2	US-09-270-767-47581	Sequence 47581, A

258	54.5	11.8	221	2	US-09-270-767-31937	Sequence 31937, A	331	54	11.7	417	4	PCT-US94-07280-19	Sequence 19, Appl
259	54.5	11.8	221	2	US-09-270-767-47154	Sequence 47154, A	332	54	11.7	417	4	PCT-US95-01087-19	Sequence 19, Appl
260	54.5	11.8	220	2	US-09-902-540-11028	Sequence 11028, A	333	54	11.7	434	1	US-08-188-281B-10	Sequence 10, Appl
261	54.5	11.8	257	2	US-08-875-811-59	Sequence 59, Appl	334	54	11.7	434	4	PCT-US94-07280-10	Sequence 10, Appl
262	54.5	11.8	261	2	US-09-634-238-278	Sequence 278, Appl	335	54	11.7	434	4	PCT-US95-01087-10	Sequence 10, Appl
263	54.5	11.8	384	1	US-08-675-650B-4	Sequence 4, Appl	336	54	11.7	441	1	US-08-188-281B-11	Sequence 21, Appl
264	54.5	11.8	384	1	US-08-675-650B-6	Sequence 6, Appl	337	54	11.7	441	4	PCT-US94-07280-21	Sequence 21, Appl
265	54.5	11.8	384	2	US-08-907-608-2	Sequence 2, Appl	338	54	11.7	441	4	PCT-US95-01087-11	Sequence 21, Appl
266	54.5	11.8	384	2	US-08-907-608-4	Sequence 4, Appl	339	54	11.7	443	2	US-09-461-325-147	Sequence 147, Appl
267	54.5	11.8	384	2	US-09-059-759-10	Sequence 10, Appl	340	54	11.7	443	2	US-10-012-542-147	Sequence 147, Appl
268	54.5	11.8	384	2	US-09-354-231B-2	Sequence 2, Appl	341	54	11.7	443	2	US-10-115-123-117	Sequence 147, Appl
269	54.5	11.8	384	2	US-09-354-231B-4	Sequence 4, Appl	342	54	11.7	447	1	US-08-188-281B-20	Sequence 20, Appl
270	54.5	11.8	384	2	US-09-128-602B-2	Sequence 2, Appl	343	54	11.7	447	4	PCT-US94-07280-20	Sequence 20, Appl
271	54.5	11.8	384	2	US-09-128-602B-4	Sequence 4, Appl	344	54	11.7	447	4	PCT-US95-01087-20	Sequence 20, Appl
272	54.5	11.8	384	2	US-09-482-287-2	Sequence 2, Appl	345	54	11.7	453	1	US-08-188-281B-16	Sequence 16, Appl
273	54.5	11.8	384	2	US-09-482-287-4	Sequence 4, Appl	346	54	11.7	453	4	PCT-US94-07280-16	Sequence 16, Appl
274	54.5	11.8	384	2	US-09-966-888-2	Sequence 2, Appl	347	54	11.7	453	4	PCT-US95-01087-16	Sequence 16, Appl
275	54.5	11.8	384	2	US-09-966-888-4	Sequence 4, Appl	348	54	11.7	478	2	US-09-489-039A-7367	Sequence 7367, Appl
276	54.5	11.8	384	2	US-09-995-297-2	Sequence 2, Appl	349	54	11.7	490	1	US-08-188-281B-15	Sequence 15, Appl
277	54.5	11.8	384	2	US-09-995-297-4	Sequence 4, Appl	350	54	11.7	490	4	PCT-US94-07280-15	Sequence 15, Appl
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279	54.5	11.8	446	2	US-09-543-681A-5864	Sequence 5864, Ap	352	54	11.7	493	2	US-09-170-98A-2	Sequence 2, Appl
280	54.5	11.8	477	2	US-09-489-039A-10570	Sequence 10570, A	353	54	11.7	518	2	US-09-540-235-348	Sequence 348, Ap
281	54.5	11.8	481	2	US-09-724-623-77	Sequence 77, Appl	354	54	11.7	880	2	US-09-538-092-601	Sequence 601, Appl
282	54.5	11.8	613	2	US-09-328-352-7962	Sequence 7962, Ap	355	54	11.7	891	2	US-09-252-991A-28689	Sequence 28689, A
283	54.5	11.8	752	1	US-09-328-352-6860	Sequence 6860, Ap	356	54	11.7	1036	2	US-09-902-540-14218	Sequence 14218, A
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285	54.5	11.8	752	1	US-08-735-716-2	Sequence 2, Appl	358	53.5	11.6	72	2	US-09-188-930-182	Sequence 182, Appl
286	54.5	11.8	752	1	US-08-555-568B-2	Sequence 2, Appl	359	53.5	11.6	221	2	US-09-464-535-22	Sequence 22, Appl
287	54.5	11.8	752	2	US-09-519-223-2	Sequence 2, Appl	360	53.5	11.6	244	1	US-08-361-395-1	Sequence 1, Appl
288	54.5	11.8	752	2	US-09-927-180-2	Sequence 2, Appl	361	53.5	11.6	272	2	US-09-618-259-11	Sequence 11, Appl
289	54.5	11.8	752	4	PCT-US95-08069-2	Sequence 2, Appl	362	53.5	11.6	272	2	US-09-583-110-3866	Sequence 3866, Ap
290	54.5	11.8	765	2	US-09-949-016-7844	Sequence 7844, Ap	363	53.5	11.6	284	2	US-09-902-540-16417	Sequence 16417, A
291	54.5	11.8	780	2	US-09-902-540-10063	Sequence 10063, A	364	53.5	11.6	308	2	US-09-252-991A-21655	Sequence 21655, A
292	54.5	11.8	895	1	US-08-123-161A-8	Sequence 8, Appl	365	53.5	11.6	308	2	US-09-489-039A-14278	Sequence 14278, A
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294	54.5	11.8	895	2	US-09-949-016-6490	Sequence 6490, Ap	367	53.5	11.6	325	2	US-09-949-016-7713	Sequence 7713, Ap
295	54.5	11.8	895	2	US-08-489-039A-13666	Sequence 13666, A	368	53.5	11.6	359	2	US-08-637-670-37	Sequence 37, Appl
296	54.5	11.8	920	2	US-09-949-016-7178	Sequence 7178, Ap	369	53.5	11.6	382	2	US-09-489-039A-13666	Sequence 13666, A
297	54	11.7	135	1	US-08-188-281B-6	Sequence 6, Appl	370	53.5	11.6	407	2	US-09-710-278-1578	Sequence 1578, Ap
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299	54	11.7	135	4	PCT-US95-01087-6	Sequence 6, Appl	372	53.5	11.6	410	2	US-09-189-627A-10	Sequence 10, Appl
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303	54	11.7	178	2	US-09-936-588-42	Sequence 42, Appl	376	53.5	11.6	438	2	US-08-486-099-105	Sequence 105, Ap
304	54	11.7	221	4	US-08-188-281B-2	Sequence 2, Appl	377	53.5	11.6	438	2	US-08-360-107A-115	Sequence 115, Ap
305	54	11.7	221	4	PCT-US94-07280-2	Sequence 2, Appl	378	53.5	11.6	438	2	US-08-484-222B-105	Sequence 105, Ap
306	54	11.7	221	4	PCT-US95-01087-2	Sequence 2, Appl	379	53.5	11.6	438	2	US-08-919-597-105	Sequence 105, Ap
307	54	11.7	241	2	US-09-005-298-46	Sequence 46, Appl	380	53.5	11.6	438	2	US-08-475-668A-105	Sequence 105, Ap
308	54	11.7	241	2	US-08-768-619-46	Sequence 46, Appl	381	53.5	11.6	438	2	US-08-485-551A-105	Sequence 105, Ap
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313	54	11.7	346	2	US-09-589-184-329	Sequence 329, Ap	386	53.5	11.6	438	2	US-08-485-546A-105	Sequence 105, Ap
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315	54	11.7	346	2	US-10-017-754-329	Sequence 329, Ap	388	53.5	11.6	438	2	US-08-484-741-105	Sequence 105, Ap
316	54	11.7	346	2	US-09-651-563-329	Sequence 329, Ap	389	53.5	11.6	440	2	US-09-134-001C-3286	Sequence 3286, Ap
317	54	11.7	346	2	US-09-519-642-329	Sequence 329, Ap	390	53.5	11.6	495	2	US-09-275-252A-5	Sequence 5, Appl
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319	54	11.7	377	1	PCT-US94-07280-17	Sequence 17, Appl	392	53.5	11.6	550	2	US-09-873-233A-18	Sequence 18, Appl
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321	54	11.7	377	4	PCT-US95-01087-17	Sequence 17, Appl	394	53.5	11.6	550	2	US-09-873-233A-18	Sequence 18, Appl
322	54	11.7	395	2	US-09-540-236-2520	Sequence 2520, Ap	395	53.5	11.6	550	2	US-09-873-233A-20	Sequence 20, Appl
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324	54	11.7	397	4	PCT-US94-07280-11	Sequence 11, Appl	397	53.5	11.6	898	2	US-10-449-315-11	Sequence 11, Appl
325	54	11.7	397	4	PCT-US95-01087-11	Sequence 11, Appl	398	53	11.5	68	2	US-09-243-675-3	Sequence 3, Appl
326	54	11.7	410	1	US-08-188-281B-18	Sequence 18, Appl	399	53	11.5	78	2	US-09-749-637A-328	Sequence 328, Ap
327	54	11.7	410	4	PCT-US94-07280-18	Sequence 18, Appl	400	53	11.5	165	2	US-10-104-047-2538	Sequence 2538, Ap
328	54	11.7	410	4	PCT-US95-01087-18	Sequence 18, Appl	401	53	11.5	223	2	US-09-605-703B-2326	Sequence 2326, Ap
329	54	11.7	412	2	US-09-489-039A-9118	Sequence 9118, Ap	402	53	11.5	225	2	US-09-543-681A-4579	Sequence 4579, Ap
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405	53	11.5	299	2	US-09-252-991A-24215	Sequence 24215, A	478	52.5	11.4	410	1	US-08-602-846-2	Sequence 2, Appli
406	53	11.5	319	2	US-09-134-000C-6061	Sequence 6061, Ap	479	52.5	11.4	410	2	US-09-078-596-2	Sequence 2, Appli
407	53	11.5	348	2	US-09-134-001C-4857	Sequence 4857, Ap	480	52.5	11.4	410	2	US-09-189-627A-11	Sequence 11, Appli
408	53	11.5	355	2	US-09-902-540-14706	Sequence 14706, A	481	52.5	11.4	410	2	US-09-710-661-11	Sequence 11, Appli
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411	53	11.5	377	1	US-08-429-964-78	Sequence 78, Appli	484	52.5	11.4	468	2	US-09-602-787A-612	Sequence 612, Ap
412	53	11.5	377	2	US-09-538-092-1199	Sequence 1199, Ap	485	52.5	11.4	483	2	US-09-949-016-7773	Sequence 7773, Ap
413	53	11.5	407	2	US-09-489-039A-13350	Sequence 13350, A	486	52.5	11.4	523	2	US-09-538-092-5771	Sequence 577, Ap
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415	53	11.5	460	2	US-09-489-039A-13505	Sequence 13505, A	488	52.5	11.4	525	2	US-08-888-950-16	Sequence 16, Appli
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418	53	11.5	476	2	US-09-489-039A-12217	Sequence 12217, A	491	52.5	11.4	525	2	US-09-885-876-16	Sequence 16, Appli
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422	53	11.5	563	2	US-09-949-016-8277	Sequence 8277, Ap	495	52.5	11.4	609	2	US-09-515-039-1	Sequence 1, Appli
423	53	11.5	574	2	US-09-248-796A-16849	Sequence 16849, A	496	52.5	11.4	693	2	US-09-107-532A-5110	Sequence 5110, Ap
424	53	11.5	580	2	US-09-489-039A-8096	Sequence 8096, Ap	497	52.5	11.4	706	2	US-09-949-016-9666	Sequence 9666, Ap
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430	53	11.5	896	2	US-09-585-858-17	Sequence 17, Appli	503	52.5	11.4	1000	2	US-09-352-159-25	Sequence 25, Appli
431	53	11.5	896	2	US-10-270-878-17	Sequence 17, Appli	504	52.5	11.4	1000	2	US-09-352-159-25	Sequence 25, Appli
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433	53	11.5	1070	2	US-09-961-403-3	Sequence 3, Appli	506	52.5	11.4	1000	2	US-09-770-564A-25	Sequence 25, Appli
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435	53	11.5	1238	2	US-09-904-065-2	Sequence 2, Appli	508	52.5	11.4	1101	2	US-08-331-625A-52	Sequence 52, Appli
436	53	11.5	1238	2	US-09-904-065-14	Sequence 14, Appli	509	52.5	11.4	1101	2	US-08-331-625A-54	Sequence 54, Appli
437	53	11.5	1240	1	US-08-680-326-37	Sequence 37, Appli	510	52.5	11.4	1101	2	US-09-494-151-52	Sequence 52, Appli
438	53	11.5	1240	2	US-09-904-065-4	Sequence 4, Appli	511	52.5	11.4	1101	2	US-09-494-151-54	Sequence 54, Appli
439	53	11.5	1240	2	US-09-904-065-15	Sequence 15, Appli	512	52.5	11.4	1101	2	US-09-972-484-52	Sequence 52, Appli
440	53	11.5	1326	2	US-09-949-016-6806	Sequence 6806, Ap	513	52.5	11.4	1205	2	US-09-972-484-54	Sequence 54, Appli
441	53	11.5	1339	2	US-09-949-016-10448	Sequence 10448, A	514	52.5	11.4	1279	2	US-09-421-522-51	Sequence 11, Appli
442	53	11.5	1438	2	US-09-949-016-8315	Sequence 8315, Ap	515	52.5	11.4	1452	2	US-09-489-039A-13602	Sequence 13602, A
443	52.5	11.4	21	2	US-09-962-756-592	Sequence 592, App	516	52.5	11.4	1452	2	US-08-331-625A-1	Sequence 2, Appli
444	52.5	11.4	71	2	US-09-369-247-79	Sequence 79, Appli	517	52.5	11.4	1452	2	US-09-494-151-2	Sequence 2, Appli
445	52.5	11.4	123	2	US-10-062-548-79	Sequence 79, Appli	518	52.5	11.4	1452	4	US-09-972-484-2	Sequence 2, Appli
446	52.5	11.4	126	2	US-08-331-625A-9	Sequence 4652, Ap	519	52.5	11.4	1452	4	PCT-US93-0438A-18	Sequence 18, Appli
447	52.5	11.4	126	2	US-08-331-625A-9	Sequence 9, Appli	520	52.5	11.4	1453	1	PCT-US93-04692-2	Sequence 2, Appli
448	52.5	11.4	126	2	US-09-494-151-9	Sequence 9, Appli	521	52.5	11.4	2037	2	US-08-308-872B-6	Sequence 6, Appli
449	52.5	11.4	158	2	US-09-972-484-9	Sequence 9, Appli	522	52.5	11.4	2037	2	US-09-306-998-3	Sequence 3, Appli
450	52.5	11.4	158	2	US-09-464-535-8	Sequence 8, Appli	523	52.5	11.4	2037	2	US-09-949-016-3365	Sequence 9665, Ap
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453	52.5	11.4	236	2	US-09-270-767-4948	Sequence 44948, A	526	52	11.3	127	2	US-09-328-352-4209	Sequence 4209, Ap
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455	52.5	11.4	251	2	US-09-494-151-59	Sequence 59, Appli	528	52	11.3	136	2	US-09-270-767-99814	Sequence 3814, A
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458	52.5	11.4	384	2	US-09-354-231B-6	Sequence 6, Appli	531	52	11.3	175	2	US-09-107-433-1565	Sequence 3565, Ap
459	52.5	11.4	384	2	US-09-354-231B-8	Sequence 8, Appli	532	52	11.3	216	2	US-09-270-767-46710	Sequence 46710, A
460	52.5	11.4	384	2	US-09-354-231B-10	Sequence 10, Appli	533	52	11.3	231	2	US-09-107-362A-3711	Sequence 3711, Ap
461	52.5	11.4	384	2	US-09-354-231B-12	Sequence 12, Appli	534	52	11.3	260	2	US-09-303-518D-432	Sequence 432, App
462	52.5	11.4	384	2	US-09-133-962A-4	Sequence 4, Appli	535	52	11.3	260	2	US-09-025-059-3	Sequence 3, Appli
463	52.5	11.4	384	2	US-09-128-602B-6	Sequence 6, Appli	536	52	11.3	260	2	US-08-888-429A-26	Sequence 26, Appli
464	52.5	11.4	384	2	US-09-128-602B-8	Sequence 8, Appli	537	52	11.3	260	2	US-09-593-653-36	Sequence 26, Appli
465	52.5	11.4	384	2	US-09-128-602B-10	Sequence 10, Appli	538	52	11.3	260	2	US-09-618-259-8	Sequence 8, Appli
466	52.5	11.4	384	2	US-09-128-602B-12	Sequence 12, Appli	539	52	11.3	262	2	US-09-454-279-16	Sequence 16, Appli
467	52.5	11.4	384	2	US-09-482-287-6	Sequence 6, Appli	540	52	11.3	267	2	US-09-303-518B-434	Sequence 434, App
468	52.5	11.4	384	2	US-09-966-888-6	Sequence 6, Appli	541	52	11.3	304	2	US-09-248-796A-17580	Sequence 17580, A
469	52.5	11.4	384	2	US-09-995-297-6	Sequence 6, Appli	542	52	11.3	312	2	US-09-543-681A-7290	Sequence 7290, Ap
470	52.5	11.4	384	2	US-09-995-297-8	Sequence 8, Appli	543	52	11.3	336	2	US-09-543-681A-6689	Sequence 6689, Ap
471	52.5	11.4	384	2	US-09-995-297-10	Sequence 10, Appli	544	52	11.3	350	2	US-09-543-681A-10582	Sequence 10582, A
472	52.5	11.4	384	2	US-09-995-297-12	Sequence 12, Appli	545	52	11.3	371	2	US-09-543-681A-4618	Sequence 4618, Ap
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474	52.5	11.4	384	2	US-10-116-212A-4	Sequence 4, Appli	547	52	11.3	380	2	US-08-888-429A-30	Sequence 30, Appli
475	52.5	11.4	396	2	US-09-198-452A-147	Sequence 147, App	548	52	11.3	387	2	US-09-593-653-30	Sequence 30, Appli
476	52.5	11.4	410	1	US-08-723-415B-11	Sequence 11, Appli	549	52	11.3	389	2	US-09-252-991A-22112	Sequence 22112, A

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552	52	11.3	419	2	US-08-888-429A-28	Sequence 28, Appl	635	51.5	11.2	383	2	US-09-225-024-4	Sequence 4, Appl
553	52	11.3	419	2	US-09-446-754-6	Sequence 6, Appl	636	51.5	11.2	384	2	US-08-530-862B-4	Sequence 4, Appl
554	52	11.3	419	2	US-09-206-166-2	Sequence 5, Appl	637	51.5	11.2	384	2	US-08-597-333D-4	Sequence 4, Appl
555	52	11.3	419	2	US-09-206-166-5	Sequence 5, Appl	638	51.5	11.2	384	2	US-09-885-189-4	Sequence 4, Appl
556	52	11.3	419	2	US-09-593-653-28	Sequence 28, Appl	639	51.5	11.2	390	1	US-08-416-756A-5	Sequence 5, Appl
557	52	11.3	420	1	US-08-864-804-1	Sequence 1, Appl	640	51.5	11.2	390	2	US-08-880-865-5	Sequence 5, Appl
558	52	11.3	433	2	US-09-949-016-7636	Sequence 7636, Ap	641	51.5	11.2	407	2	US-08-753-007A-6	Sequence 6, Appl
559	52	11.3	435	2	US-09-446-754-2	Sequence 2, Appl	642	51.5	11.2	407	2	US-09-398-496-6	Sequence 6, Appl
560	52	11.3	453	2	US-08-888-429A-32	Sequence 32, Appl	643	51.5	11.2	429	2	US-08-311-731A-287	Sequence 287, Ap
561	52	11.3	453	2	US-09-593-653-32	Sequence 32, Appl	644	51.5	11.2	453	2	US-09-540-236-3464	Sequence 3464, Ap
562	52	11.3	468	2	US-09-446-754-4	Sequence 4, Appl	645	51.5	11.2	495	2	US-09-270-767-44726	Sequence 44726, A
563	52	11.3	475	2	US-09-446-754-10	Sequence 10, Appl	646	51.5	11.2	501	2	US-08-845-546-2	Sequence 2, Appl
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565	52	11.3	482	2	US-09-489-039A-9909	Sequence 9909, Ap	648	51.5	11.2	522	2	US-09-549-519-8	Sequence 496-6
566	52	11.3	521	2	US-08-669-656A-4	Sequence 4, Appl	649	51.5	11.2	549	2	US-09-345-473E-32	Sequence 32, Appl
567	52	11.3	536	2	US-09-134-001C-3363	Sequence 3363, Ap	650	51.5	11.2	549	2	US-09-862-027-32	Sequence 32, Appl
568	52	11.3	628	2	US-09-602-787A-550	Sequence 550, App	651	51.5	11.2	550	1	US-08-348-891A-5	Sequence 5, Appl
569	52	11.3	628	2	US-09-602-787A-666	Sequence 666, App	652	51.5	11.2	550	1	US-08-905-817-5	Sequence 5, Appl
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571	52	11.3	1194	2	US-09-949-016-9803	Sequence 9803, Ap	654	51.5	11.2	563	2	US-10-046-232-24	Sequence 24, Appl
572	52	11.3	1195	2	US-09-949-016-6535	Sequence 6535, Ap	655	51.5	11.2	567	2	US-09-252-991A-28481	Sequence 28481, A
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574	52	11.3	1956	2	US-08-843-417-2	Sequence 2, Appl	657	51.5	11.2	630	2	US-09-252-991A-18033	Sequence 18033, A
575	52	11.3	1956	2	US-09-527-013-2	Sequence 2, Appl	658	51.5	11.2	707	2	US-09-228-986-80	Sequence 80, Appl
576	52	11.3	1957	2	US-08-669-656A-2	Sequence 2, Appl	659	51.5	11.2	707	2	US-10-101-464A-80	Sequence 11, Appl
577	52	11.3	1957	2	US-08-669-656A-8	Sequence 8, Appl	660	51.5	11.2	760	2	US-09-589-892B-11	Sequence 11, Appl
578	52	11.3	2057	2	US-09-499-203-2	Sequence 2, Appl	661	51.5	11.2	808	2	US-10-104-047-2654	Sequence 2654, Ap
579	52	11.3	2132	2	US-08-669-656A-6	Sequence 6, Appl	662	51.5	11.2	848	2	US-08-976-225-10	Sequence 10, Appl
580	51.5	11.2	115	2	US-09-513-999C-7866	Sequence 7866, Ap	663	51.5	11.2	869	1	US-08-483-101-15	Sequence 15, Appl
581	51.5	11.2	123	1	US-08-180-209B-19	Sequence 19, Appl	664	51.5	11.2	1451	1	US-08-308-872B-4	Sequence 4, Appl
582	51.5	11.2	123	1	US-08-385-745-19	Sequence 19, Appl	665	51.5	11.2	1454	2	US-08-392-459-32	Sequence 32, Appl
583	51.5	11.2	123	2	US-08-485-388-19	Sequence 19, Appl	666	51.5	11.2	1454	2	US-09-854-799-32	Sequence 32, Appl
584	51.5	11.2	123	2	US-08-474-853-19	Sequence 19, Appl	667	51.5	11.2	1454	4	PCT-US91-08555-32	Sequence 32, Appl
585	51.5	11.2	123	2	US-09-166-205B-19	Sequence 19, Appl	668	51.5	11.2	1454	4	PCT-US93-04384-12	Sequence 12, Appl
586	51.5	11.2	123	2	US-10-104-047-2234	Sequence 2234, Ap	669	51.5	11.2	1454	4	PCT-US93-04384-14	Sequence 14, Appl
587	51.5	11.2	123	4	PCT-US94-02629-19	Sequence 19, Appl	670	51.5	11.2	1454	4	PCT-US93-04384-16	Sequence 16, Appl
588	51.5	11.2	134	2	US-09-605-703B-1756	Sequence 1756, Ap	671	51.5	11.2	1454	4	PCT-US93-04384-47	Sequence 47, Appl
589	51.5	11.2	185	2	US-09-252-991A-20175	Sequence 20175, A	672	51.5	11.2	2539	2	US-09-413-814-42	Sequence 42, Appl
590	51.5	11.2	187	2	US-09-949-016-9179	Sequence 9179, Ap	673	51	11.1	86	2	US-08-654-737B-2	Sequence 2, Appl
591	51.5	11.2	211	2	US-09-130-491-4	Sequence 4, Appl	674	51	11.1	109	2	US-09-198-452A-11	Sequence 11, Appl
592	51.5	11.2	211	2	US-09-603-552-12	Sequence 12, Appl	675	51	11.1	109	2	US-09-438-185A-2	Sequence 2, Appl
593	51.5	11.2	211	2	US-09-886-683A-4	Sequence 4, Appl	676	51	11.1	119	2	US-09-270-767-32131	Sequence 32131, A
594	51.5	11.2	212	1	US-09-949-016-6992	Sequence 6992, Ap	677	51	11.1	141	2	US-09-543-681A-6396	Sequence 6396, Ap
595	51.5	11.2	212	1	US-08-461-859-35	Sequence 35, Appl	678	51	11.1	205	2	US-09-605-703B-1998	Sequence 1998, Ap
596	51.5	11.2	212	2	US-09-917-254-62	Sequence 62, Appl	679	51	11.1	211	2	US-09-248-796A-20685	Sequence 20685, A
597	51.5	11.2	212	2	US-08-871-572B-13	Sequence 13, Appl	680	51	11.1	214	1	US-08-277-231A-14	Sequence 14, Appl
598	51.5	11.2	224	2	US-09-252-991A-30410	Sequence 30410, A	681	51	11.1	214	1	US-08-473-750-3	Sequence 3, Appl
599	51.5	11.2	240	2	US-10-076-069-4	Sequence 4, Appl	682	51	11.1	214	1	US-08-277-231A-2	Sequence 2, Appl
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602	51.5	11.2	250	2	US-09-818-780-17	Sequence 17, Appl	685	51	11.1	217	1	US-08-473-750-5	Sequence 5, Appl
603	51.5	11.2	268	2	US-09-818-780-94	Sequence 94, Appl	686	51	11.1	217	1	US-08-477-326-1	Sequence 1, Appl
604	51.5	11.2	268	2	US-10-004-860-1116	Sequence 1116, Ap	687	51	11.1	217	1	US-08-477-326-5	Sequence 5, Appl
605	51.5	11.2	292	2	US-09-404-860-1116	Sequence 1116, Ap	688	51	11.1	217	1	US-09-252-991A-29014	Sequence 29014, A
606	51.5	11.2	292	2	US-08-581-148C-12	Sequence 12, Appl	689	51	11.1	222	2	US-09-328-352-7370	Sequence 7370, Ap
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608	51.5	11.2	319	2	PCT-US93-08528-73	Sequence 73, Appl	691	51	11.1	294	2	US-09-949-016-8751	Sequence 8751, Ap
609	51.5	11.2	334	4	US-08-416-756A-2	Sequence 2, Appl	692	51	11.1	301	2	US-08-888-429A-18	Sequence 18, Appl
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611	51.5	11.2	369	2	US-09-949-016-9073	Sequence 9073, Ap	694	51	11.1	321	2	US-09-290-586A-22	Sequence 22, Appl
612	51.5	11.2	371	2	US-08-845-566-3	Sequence 3, Appl	695	51	11.1	326	2	US-09-489-039A-10966	Sequence 10966, A
613	51.5	11.2	381	1	US-08-467-948A-28	Sequence 28, Appl	696	51	11.1	328	2	US-09-134-001C-3815	Sequence 3815, Ap
614	51.5	11.2	381	1	US-08-852-824-18	Sequence 18, Appl	697	51	11.1	330	2	US-09-949-016-8751	Sequence 18, Appl
615	51.5	11.2	381	2	US-08-467-947A-28	Sequence 28, Appl	698	51	11.1	336	2	US-08-888-429A-18	Sequence 18, Appl
616	51.5	11.2	381	2	US-09-731-030A-17	Sequence 17, Appl	699	51	11.1	346	2	US-09-198-452A-60	Sequence 60, Appl
617	51.5	11.2	381	2	US-09-518-383-18	Sequence 18, Appl	700	51	11.1	346	2	US-09-593-653-18	Sequence 18, Appl
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619	51.5	11.2	381	4	US-09-542-733-2	Sequence 4, Appl	702	51	11.1	354	2	US-08-390-162-4	Sequence 4, Appl
620	51.5	11.2	382	2	US-09-262-477-2	Sequence 2, Appl	703	51	11.1	361	1	US-08-685-945B-4	Sequence 4, Appl
621	51.5	11.2	382	2	US-09-169-205D-21	Sequence 21, Appl	704	51	11.1	361	1	US-08-390-162-2	Sequence 2, Appl
622	51.5	11.2	382	2			705	51	11.1	365	1		

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767	51	11.1	365	2	US-09-949-016-9075	Sequence 9075, Ap	780	50.5	11.0	529	2	US-09-169-717E-39	Sequence 39, Appli
768	51	11.1	370	2	US-09-489-039A-11515	Sequence 11515, A	781	50.5	11.0	529	2	US-10-011-436-4	Sequence 4, Appli
769	51	11.1	380	2	US-09-902-540-15775	Sequence 15775, A	782	50.5	11.0	529	2	US-08-533-895A-39	Sequence 39, Appli
770	51	11.1	383	2	US-08-530-862B-7	Sequence 7, Appli	783	50.5	11.0	537	2	US-08-540-922D-12	Sequence 12, Appli
771	51	11.1	384	2	US-08-597-313D-7	Sequence 7, Appli	784	50.5	11.0	550	1	US-08-279-700-18	Sequence 18, Appli
772	51	11.1	384	2	US-09-885-189-7	Sequence 7, Appli	785	50.5	11.0	550	1	US-08-279-700-18	Sequence 18, Appli
773	51	11.1	430	2	US-09-902-540-1684	Sequence 12684, A	786	50.5	11.0	550	1	US-08-279-700-22	Sequence 22, Appli
774	51	11.1	438	2	US-09-107-532A-5677	Sequence 5677, Ap	787	50.5	11.0	560	1	US-07-891-942G-5	Sequence 5, Appli
775	51	11.1	451	2	US-09-489-039A-8949	Sequence 8949, Ap	788	50.5	11.0	566	2	US-09-491-522-7	Sequence 7, Appli
776	51	11.1	475	2	US-09-489-039A-8862	Sequence 8862, Ap	789	50.5	11.0	566	2	US-09-949-016-7010	Sequence 7010, Ap
777	51	11.1	485	2	US-10-140-372-12	Sequence 12, Appli	790	50.5	11.0	566	2	US-09-949-016-8505	Sequence 8505, Ap
778	51	11.1	485	2	US-09-438-185A-43	Sequence 43, Appli	791	50.5	11.0	566	2	US-09-949-002-452	Sequence 452, App
779	51	11.1	490	2	US-09-438-185A-1032	Sequence 1032, Ap	792	50.5	11.0	596	2	US-09-252-991A-22689	Sequence 22689, A
780	51	11.1	534	2	US-09-605-703B-1142	Sequence 1142, Ap	793	50.5	11.0	614	2	US-09-949-016-10772	Sequence 10772, A
781	51	11.1	584	2	US-09-107-532A-4564	Sequence 4564, Ap	794	50.5	11.0	757	2	US-09-902-540-11380	Sequence 11380, A
782	51	11.1	590	2	US-09-248-796A-26874	Sequence 26874, A	795	50.5	11.0	867	2	US-09-839-894-6	Sequence 11380, A
783	51	11.1	598	2	US-09-248-796A-19180	Sequence 19180, A	796	50.5	11.0	974	2	US-08-938-291A-4	Sequence 6, Appli
784	51	11.1	677	2	US-09-252-991A-30406	Sequence 20406, A	797	50.5	11.0	974	2	US-09-589-619-4	Sequence 4, Appli
785	51	11.1	677	2	US-08-046-508-2	Sequence 2, Appli	798	50.5	11.0	1106	2	US-09-134-000C-6136	Sequence 6136, Ap
786	51	11.1	749	2	US-09-250-083C-2	Sequence 2, Appli	799	50.5	11.0	1163	1	US-08-173-497-4	Sequence 4, Appli
787	51	11.1	822	2	US-09-248-796A-19917	Sequence 19917, A	800	50.5	11.0	1163	1	US-08-286-889-4	Sequence 4, Appli
788	51	11.1	866	1	US-08-386-727-8	Sequence 8, Appli	801	50.5	11.0	1163	1	US-08-485-618-4	Sequence 4, Appli
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792	51	11.1	967	2	US-09-659-786-201	Sequence 201, App	805	50.5	11.0	1163	1	US-08-943-363-4	Sequence 4, Appli
793	51	11.1	1049	2	US-09-854-845-2	Sequence 2, Appli	806	50.5	11.0	1163	1	US-08-476-062A-44	Sequence 44, Appli
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798	51	11.1	1956	2	US-09-527-013-10	Sequence 10, Appli	811	50.5	11.0	1211	2	US-09-491-522-5	Sequence 5, Appli
799	51	11.1	26	2	US-09-962-756-1658	Sequence 1658, Ap	812	50.5	11.0	1211	2	US-09-949-016-11401	Sequence 11401, A
799	50.5	11.0	26	2	US-09-605-703B-960	Sequence 960, App	813	50.5	11.0	1211	2	US-09-949-002-401	Sequence 401, App
799	50.5	11.0	87	2	US-09-605-703B-962	Sequence 962, App	814	50.5	11.0	1211	2	US-09-949-002-555	Sequence 555, App
799	50.5	11.0	87	2	US-10-104-047-2706	Sequence 2706, Ap	815	50.5	11.0	1245	2	US-09-252-991A-30935	Sequence 30935, A
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799	50.5	11.0	207	1	US-08-851-896-15	Sequence 15, Appli	820	50.5	11.0	3169	1	US-08-477-451-6	Sequence 6, Appli
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799	50.5	11.0	254	2	US-09-605-703B-242	Sequence 242, App	825	50	10.8	92	2	US-10-191-732-8	Sequence 8, Appli
799	50.5	11.0	263	2	US-08-463-115-93	Sequence 93, Appli	826	50	10.8	93	2	US-09-148-545-256	Sequence 256, App
799	50.5	11.0	264	1	US-08-465-388-93	Sequence 93, Appli	827	50	10.8	93	2	US-09-621-011-156	Sequence 156, App
799	50.5	11.0	271	2	US-09-252-991A-18965	Sequence 18965, A	828	50	10.8	102	2	US-09-198-452A-475	Sequence 475, App
799	50.5	11.0	304	2	US-09-902-540-1353	Sequence 1353, A	829	50	10.8	105	2	US-09-248-796A-19711	Sequence 19711, A
799	50.5	11.0	306	2	US-09-252-991A-22181	Sequence 22181, A	830	50	10.8	119	2	US-09-482-273-264	Sequence 264, App
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799	50.5	11.0	477	2	US-09-252-991A-29825	Sequence 29825, A	847	50	10.8	308	2	US-08-815-927-18	Sequence 18, Appli
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799	50.5	11.0	529	1	US-08-370-909-19	Sequence 19, Appli	850	50	10.8	322	2	US-09-252-991A-24657	Sequence 24657, A
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854	50	10.8	356	2	US-09-125-619-13	Sequence 13, Appl	927	49.5	10.7	372	2	US-08-993-088A-20	Sequence 20, Appl
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858	50	10.8	356	2	US-10-143-024A-13	Sequence 13, Appl	931	49.5	10.7	372	2	US-09-595-459-9	Sequence 9, Appl
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860	50	10.8	356	2	US-10-222-162-13	Sequence 13, Appl	933	49.5	10.7	372	2	US-09-603-680-20	Sequence 20, Appl
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862	50	10.8	378	2	US-09-902-540-11860	Sequence 11860, A	935	49.5	10.7	372	2	US-08-899-112B-8	Sequence 8, Appl
863	50	10.8	390	2	US-09-710-279-1422	Sequence 1422, Ap	936	49.5	10.7	372	2	US-09-011-553-2	Sequence 2, Appl
864	50	10.8	427	2	US-09-902-540-15413	Sequence 15413, A	937	49.5	10.7	372	2	US-09-689-486-62	Sequence 62, Appl
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867	50	10.8	447	2	US-10-162-012-29	Sequence 29, Appl	940	49.5	10.7	380	2	US-08-860-255A-5	Sequence 5, Appl
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873	50	10.8	525	2	US-09-949-016-7407	Sequence 7407, Ap	946	49.5	10.7	427	2	US-09-328-352-6602	Sequence 6602, Ap
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879	50	10.8	641	2	US-10-461-791-13	Sequence 13, Appl	952	49.5	10.7	476	2	US-09-134-001C-3778	Sequence 3778, Ap
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883	50	10.8	1086	2	US-09-653-274-4	Sequence 4, Appl	956	49.5	10.7	507	2	US-10-214-811-20	Sequence 20, Appl
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885	50	10.8	1309	2	US-09-862-027-82	Sequence 82, Appl	958	49.5	10.7	532	2	US-10-214-811-20	Sequence 20, Appl
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891	49.5	10.7	66	2	US-09-513-999C-7224	Sequence 7224, Ap	977	49.5	10.7	597	2	US-09-252-991A-32657	Sequence 32657, A
892	49.5	10.7	160	2	US-09-732-210-304	Sequence 304, App	978	49.5	10.7	607	2	US-09-252-991A-32653	Sequence 32643, A
893	49.5	10.7	160	2	US-09-107-532A-5111	Sequence 5111, Ap	979	49.5	10.7	637	2	US-09-569-611C-35	Sequence 35, Appl
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895	49.5	10.7	172	2	US-09-062-126-2	Sequence 2, Appl	981	49.5	10.7	647	2	US-09-398-496-32	Sequence 32, Appl
896	49.5	10.7	193	2	US-09-475-316A-78	Sequence 78, Appl	988	49.5	10.7	660	2	US-09-949-016-643	Sequence 6843, Ap
897	49.5	10.7	193	2	US-09-704-640-78	Sequence 78, Appl	993	49.5	10.7	660	2	US-09-689-486-58	Sequence 58, Appl
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903	49.5	10.7	252	1	US-07-885-089B-7	Sequence 7, Appl	1002	49.5	10.7	1121	2	US-08-915-048A-2	Sequence 2, Appl
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908	49.5	10.7	265	2	US-09-780-016-8	Sequence 8, Appl	1007	49.5	10.6	118	2	US-09-056-556-231	Sequence 231, App
909	49.5	10.7	265	2	US-10-214-811-8	Sequence 8, Appl	1008	49.5	10.6	118	2	US-09-072-586-226	Sequence 226, App
910	49.5	10.7	265	2	US-10-766-074-8	Sequence 8, Appl	1009	49.5	10.6	118	2	US-09-072-586-226	Sequence 226, App
911	49.5	10.7	268	2	US-09-716-964B-156	Sequence 156, App	1010	49.5	10.6	118	2	US-10-193-002-226	Sequence 226, App
912	49.5	10.7	290	2	US-09-780-016-6	Sequence 6, Appl	1011	49.5	10.6	118	2	US-10-084-843-231	Sequence 231, App
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920	49.5	10.7	324	2	US-09-602-787A-2840	Sequence 484, App	1019	49.5	10.6	195	2	US-09-421-818-24	Sequence 24, Appl
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1028	49	10.6	231	2	US-09-893-737-1544	Sequence 154, App	1101	49	10.6	659	2	US-10-101-464A-75	Sequence 75, Appl
1029	49	10.6	235	2	US-09-902-540-15987	Sequence 15987, A	1102	49	10.6	677	2	US-09-252-991A-32924	Sequence 32924, A
1030	49	10.6	239	2	US-08-911-014A-3	Sequence 3, Appl	1103	49	10.6	681	2	US-09-270-767-42219	Sequence 42219, A
1031	49	10.6	239	2	US-09-653-285-3	Sequence 3, Appl	1104	49	10.6	719	2	US-08-765-907A-15	Sequence 15, Appl
1032	49	10.6	249	2	US-09-813-453B-70	Sequence 70, Appl	1105	49	10.6	719	2	US-09-987-614A-15	Sequence 15, Appl
1033	49	10.6	259	2	US-09-543-681A-7362	Sequence 7362, Ap	1106	49	10.6	722	2	US-09-617-145-2	Sequence 2, Appl
1034	49	10.6	262	2	US-09-069-082-4	Sequence 4, Appl	1107	49	10.6	722	2	US-09-949-016-6418	Sequence 6418, Ap
1035	49	10.6	262	2	US-09-956-085-4	Sequence 4, Appl	1108	49	10.6	726	2	US-09-248-796A-17362	Sequence 17362, A
1036	49	10.6	262	2	US-09-956-087-4	Sequence 4, Appl	1109	49	10.6	740	2	US-09-022-983-5	Sequence 5, Appl
1037	49	10.6	263	2	US-09-489-039A-12047	Sequence 12047, A	1110	49	10.6	742	2	US-09-949-016-11569	Sequence 11569, A
1038	49	10.6	266	2	US-09-134-000C-3847	Sequence 3847, Ap	1111	49	10.6	785	2	US-09-079-030-216	Sequence 216, App
1039	49	10.6	274	2	US-09-489-039A-13041	Sequence 13041, A	1112	49	10.6	787	2	US-09-489-039A-7628	Sequence 7628, Ap
1040	49	10.6	282	2	US-09-420-592A-7	Sequence 7, Appl	1113	49	10.6	839	2	US-09-538-092-274	Sequence 274, App
1041	49	10.6	282	2	US-09-985-442-7	Sequence 7, Appl	1113	49	10.6	839	2	US-09-328-352-5527	Sequence 5527, Ap
1042	49	10.6	282	2	US-09-983-580-7	Sequence 7, Appl	1114	49	10.6	862	2	US-09-635-872A-15	Sequence 15, Appl
1043	49	10.6	291	2	US-09-902-540-15435	Sequence 15435, A	1115	49	10.6	908	2	US-09-636-077A-15	Sequence 15, Appl
1044	49	10.6	321	2	US-09-949-016-7336	Sequence 7336, Ap	1116	49	10.6	908	2	US-09-636-060C-15	Sequence 15, Appl
1045	49	10.6	331	2	US-08-765-963-1	Sequence 1, Appl	1117	49	10.6	908	2	US-09-986-552-15	Sequence 15, Appl
1046	49	10.6	332	2	US-09-328-352-4745	Sequence 4745, Ap	1118	49	10.6	908	2	US-09-636-596C-15	Sequence 15, Appl
1047	49	10.6	342	2	US-08-785-928-1	Sequence 1, Appl	1119	49	10.6	914	2	US-09-623-624-6	Sequence 6, Appl
1048	49	10.6	342	2	US-08-728-603-17	Sequence 17, Appl	1120	49	10.6	914	2	US-10-055-412B-28	Sequence 28, Appl
1049	49	10.6	345	2	US-09-328-352-4841	Sequence 4841, Ap	1121	49	10.6	908	2	US-10-306-866-15	Sequence 15, Appl
1050	49	10.6	345	2	US-08-630-172-6	Sequence 6, Appl	1122	49	10.6	908	2	US-09-895-072-15	Sequence 15, Appl
1051	49	10.6	349	2	US-09-375-419-6	Sequence 6, Appl	1123	49	10.6	914	2	US-10-023-888-9	Sequence 9, Appl
1052	49	10.6	349	2	US-09-134-001C-4004	Sequence 4004, Ap	1124	49	10.6	914	2	US-09-193-562D-28	Sequence 28, Appl
1053	49	10.6	352	2	US-08-466-343D-2	Sequence 2, Appl	1125	49	10.6	914	2	US-09-623-624-6	Sequence 6, Appl
1054	49	10.6	352	2	US-09-087-232A-13	Sequence 13, Appl	1126	49	10.6	914	2	US-10-270-595-6	Sequence 6, Appl
1055	49	10.6	352	2	US-08-861-105-14	Sequence 14, Appl	1127	49	10.6	914	2	US-10-270-595-6	Sequence 6, Appl
1056	49	10.6	352	2	US-08-575-967A-2	Sequence 2, Appl	1128	49	10.6	946	2	US-09-902-540-16817	Sequence 16817, A
1057	49	10.6	352	2	US-09-045-583-52	Sequence 52, Appl	1129	49	10.6	984	2	US-09-409-604-4	Sequence 4, Appl
1058	49	10.6	352	2	US-09-517-605-5	Sequence 5, Appl	1130	49	10.6	1070	1	US-08-633-770A-2	Sequence 2, Appl
1059	49	10.6	352	2	US-09-534-185-52	Sequence 52, Appl	1131	49	10.6	1070	2	US-09-280-197-6	Sequence 6, Appl
1060	49	10.6	352	2	US-08-833-752-5	Sequence 5, Appl	1132	49	10.6	1070	2	US-09-423-126-4	Sequence 4, Appl
1061	49	10.6	352	2	US-09-502-783A-2	Sequence 2, Appl	1133	49	10.6	1073	2	US-09-180-245-2	Sequence 2, Appl
1062	49	10.6	352	2	US-09-796-202-1	Sequence 1, Appl	1134	49	10.6	1073	2	US-09-819-249-2	Sequence 2, Appl
1063	49	10.6	352	2	US-09-938-719-5	Sequence 5, Appl	1135	49	10.6	1081	2	US-09-866-510-4	Sequence 4, Appl
1064	49	10.6	352	2	US-09-502-784A-2	Sequence 2, Appl	1136	49	10.6	1956	2	US-10-152-886-23	Sequence 23, Appl
1065	49	10.6	352	2	US-09-339-912A-2	Sequence 2, Appl	1137	49	10.6	27	2	US-09-962-756-1637	Sequence 1637, Ap
1066	49	10.6	352	2	US-08-771-276-2	Sequence 2, Appl	1138	48.5	10.5	51	2	US-10-067-422-18	Sequence 18, Appl
1067	49	10.6	352	2	US-08-771-276-20	Sequence 20, Appl	1139	48.5	10.5	57	1	US-08-358-160-103	Sequence 103, App
1068	49	10.6	352	2	US-09-939-226B-5	Sequence 5, Appl	1140	48.5	10.5	77	2	US-08-311-731A-385	Sequence 385, App
1069	49	10.6	352	2	US-09-195-662A-2	Sequence 2, Appl	1141	48.5	10.5	94	2	US-09-252-991A-29771	Sequence 29771, A
1070	49	10.6	352	2	US-09-949-002-303	Sequence 303, App	1142	48.5	10.5	112	1	US-08-284-393B-14	Sequence 14, Appl
1071	49	10.6	352	2	US-10-323-314-1	Sequence 1, Appl	1143	48.5	10.5	112	1	US-08-284-393B-14	Sequence 14, Appl
1072	49	10.6	352	2	US-09-938-703B-5	Sequence 5, Appl	1144	48.5	10.5	112	2	PCT-US95-08950-4	Sequence 4, Appl
1073	49	10.6	357	2	US-09-949-016-9074	Sequence 9074, Ap	1145	48.5	10.5	114	2	US-09-054-711C-4	Sequence 4, Appl
1074	49	10.6	358	2	US-09-543-681A-6765	Sequence 4765, Ap	1146	48.5	10.5	114	2	US-09-054-711C-5	Sequence 5, Appl
1075	49	10.6	367	4	PCT-US92-09382-2	Sequence 2, Appl	1147	48.5	10.5	114	2	US-09-679-710B-1	Sequence 1, Appl
1076	49	10.6	367	4	PCT-US92-09382-2	Sequence 2, Appl	1148	48.5	10.5	114	2	US-09-679-710B-2	Sequence 2, Appl
1077	49	10.6	378	2	US-09-949-002-552	Sequence 552, App	1149	48.5	10.5	114	2	US-09-679-710B-3	Sequence 3, Appl
1078	49	10.6	405	2	US-09-252-991A-19717	Sequence 19717, A	1150	48.5	10.5	114	2	US-09-679-710B-4	Sequence 4, Appl
1079	49	10.6	428	2	US-09-248-796A-20582	Sequence 20582, A	1151	48.5	10.5	114	2	US-09-679-710B-5	Sequence 5, Appl
1080	49	10.6	436	2	US-09-134-000C-4843	Sequence 4843, Ap	1152	48.5	10.5	114	2	US-09-679-710B-6	Sequence 6, Appl
1081	49	10.6	454	2	US-09-270-767-45646	Sequence 45646, A	1153	48.5	10.5	114	2	US-09-679-710B-7	Sequence 7, Appl
1082	49	10.6	463	1	US-08-677-049-6	Sequence 6, Appl	1154	48.5	10.5	114	2	US-09-679-710B-8	Sequence 8, Appl
1083	49	10.6	464	2	US-09-252-991A-66212	Sequence 26212, A	1155	48.5	10.5	114	2	US-09-679-710B-9	Sequence 9, Appl
1084	49	10.6	466	2	US-09-543-681A-8174	Sequence 8174, Ap	1156	48.5	10.5	114	2	US-09-679-710B-10	Sequence 10, Appl
1085	49	10.6	493	2	US-09-543-681A-6754	Sequence 6754, Ap	1157	48.5	10.5	114	2	US-09-679-710B-11	Sequence 11, Appl
1086	49	10.6	498	2	US-09-107-532A-7077	Sequence 7077, Ap	1158	48.5	10.5	114	2	US-09-679-710B-12	Sequence 12, Appl
1087	49	10.6	500	2	US-10-104-047-3456	Sequence 3456, Ap	1159	48.5	10.5	114	2	US-09-679-710B-13	Sequence 13, Appl
1088	49	10.6	501	2	US-09-252-991A-32473	Sequence 32473, A	1160	48.5	10.5	114	2	US-09-679-710B-14	Sequence 14, Appl
1089	49	10.6	513	2	US-09-488-039A-12877	Sequence 12877, A	1161	48.5	10.5	114	2	US-09-679-710B-15	Sequence 15, Appl
1090	49	10.6	513	2	US-09-488-039A-9932	Sequence 9932, Ap	1162	48.5	10.5	114	2	US-09-679-710B-16	Sequence 16, Appl
1091	49	10.6	520	2	US-09-540-236-1988	Sequence 1988, Ap	1163	48.5	10.5	114	2	US-09-679-710B-17	Sequence 17, Appl
1092	49	10.6	526	2	US-09-328-352-8024	Sequence 8024, Ap	1164	48.5	10.5	114	2	US-09-679-710B-18	Sequence 18, Appl
1093	49	10.6	548	2	US-09-543-681A-6631	Sequence 6631, Ap	1165	48.5	10.5	114	2	US-09-679-710B-19	Sequence 19, Appl
1094	49	10.6	569	2	US-09-252-991A-25628	Sequence 25628, A	1166	48.5	10.5	114	2	US-09-679-710B-20	Sequence 20, Appl
1095	49	10.6	573	2	US-09-043-709A-19	Sequence 19, Appl	1167	48.5	10.5	114	2	US-09-679-710B-21	Sequence 21, Appl
1096	49	10.6	629	1	US-08-132-990A-8	Sequence 8, Appl	1168	48.5	10.5	114	2	US-09-679-710B-22	Sequence 22, Appl
						Sequence 1, Appl	1169	48.5	10.5	114	2	US-09-938-936-1	Sequence 1, Appl

1170	48.5	10.5	114	2	US-09-938-936-3	Sequence 3, Appl1	1243	48.5	10.5	503	2	US-09-605-703B-268	Sequence 266, App
1171	48.5	10.5	114	2	US-09-938-936-4	Sequence 4, Appl1	1244	48.5	10.5	511	2	US-09-679-666B-12	Sequence 12, Appl1
1172	48.5	10.5	114	2	US-09-938-936-5	Sequence 5, Appl1	1245	48.5	10.5	515	2	US-09-438-185A-1021	Sequence 1021, Ap
1173	48.5	10.5	114	2	US-10-053-406-1	Sequence 1, Appl1	1246	48.5	10.5	524	2	US-09-902-560-16272	Sequence 16272, A
1174	48.5	10.5	114	2	US-10-053-406-2	Sequence 2, Appl1	1247	48.5	10.5	540	2	US-09-248-796A-18127	Sequence 18127, A
1175	48.5	10.5	114	2	US-10-053-406-3	Sequence 3, Appl1	1248	48.5	10.5	599	1	US-08-426-125-1	Sequence 1, Appl1
1176	48.5	10.5	114	2	US-10-053-406-4	Sequence 4, Appl1	1249	48.5	10.5	599	1	US-08-426-125-1	Sequence 1, Appl1
1177	48.5	10.5	114	2	US-10-053-406-5	Sequence 5, Appl1	1250	48.5	10.5	599	1	US-08-426-125-1	Sequence 1, Appl1
1178	48.5	10.5	114	2	US-10-053-406-6	Sequence 6, Appl1	1251	48.5	10.5	599	1	US-08-426-125-1	Sequence 1, Appl1
1179	48.5	10.5	114	2	US-10-053-406-7	Sequence 7, Appl1	1252	48.5	10.5	599	2	US-09-367-512-1	Sequence 1, Appl1
1180	48.5	10.5	114	2	US-10-053-406-8	Sequence 8, Appl1	1253	48.5	10.5	599	2	US-10-407-339-1	Sequence 1, Appl1
1181	48.5	10.5	114	2	US-10-053-406-9	Sequence 9, Appl1	1254	48.5	10.5	608	2	US-09-769-787-8	Sequence 8, Appl1
1182	48.5	10.5	114	2	US-10-053-406-10	Sequence 10, Appl1	1255	48.5	10.5	638	1	US-08-426-125-4	Sequence 4, Appl1
1183	48.5	10.5	114	2	US-10-053-406-11	Sequence 11, Appl1	1256	48.5	10.5	638	1	US-08-426-125-4	Sequence 4, Appl1
1184	48.5	10.5	114	2	US-10-053-406-12	Sequence 12, Appl1	1257	48.5	10.5	638	2	US-09-367-512-3	Sequence 3, Appl1
1185	48.5	10.5	114	2	US-10-053-406-13	Sequence 13, Appl1	1258	48.5	10.5	638	2	US-10-407-339-3	Sequence 3, Appl1
1186	48.5	10.5	114	2	US-10-053-406-14	Sequence 14, Appl1	1259	48.5	10.5	655	2	US-09-134-001C-5531	Sequence 5531, Ap
1187	48.5	10.5	114	2	US-10-053-406-15	Sequence 15, Appl1	1260	48.5	10.5	684	2	US-09-252-991A-4618	Sequence 24618, A
1188	48.5	10.5	114	2	US-10-053-406-16	Sequence 16, Appl1	1261	48.5	10.5	787	2	US-09-252-991A-28939	Sequence 28939, A
1189	48.5	10.5	114	2	US-10-053-406-17	Sequence 17, Appl1	1262	48.5	10.5	815	2	US-09-489-039A-12469	Sequence 12469, A
1190	48.5	10.5	114	2	US-10-053-406-18	Sequence 18, Appl1	1263	48.5	10.5	825	2	US-09-489-039A-8469	Sequence 8469, Ap
1191	48.5	10.5	114	2	US-10-053-406-19	Sequence 19, Appl1	1264	48.5	10.5	938	2	US-09-637-145-2	Sequence 2, Appl1
1192	48.5	10.5	114	2	US-10-053-406-20	Sequence 20, Appl1	1265	48.5	10.5	1052	2	US-09-949-016-1508	Sequence 11508, A
1193	48.5	10.5	114	2	US-10-053-406-21	Sequence 21, Appl1	1266	48.5	10.5	1161	2	US-09-327-356-2	Sequence 2, Appl1
1194	48.5	10.5	114	2	US-10-053-406-22	Sequence 22, Appl1	1267	48.5	10.5	1278	2	US-09-134-000C-6043	Sequence 6043, Ap
1195	48.5	10.5	132	1	US-08-012-543-2	Sequence 2, Appl1	1268	48.5	10.5	1501	1	US-08-447-464-3	Sequence 3, Appl1
1196	48.5	10.5	132	2	US-09-054-711C-3	Sequence 2, Appl1	1269	48.5	10.5	1501	1	US-08-716-679-3	Sequence 3, Appl1
1197	48.5	10.5	132	2	US-09-462-941-19	Sequence 19, Appl1	1270	48.5	10.5	1884	2	US-09-538-092-1329	Sequence 1329, Ap
1198	48.5	10.5	132	2	US-09-949-016-6187	Sequence 6187, Ap	1271	48.5	10.5	4545	1	US-08-804-227C-14	Sequence 14, Appl1
1199	48.5	10.5	132	4	PCT-US93-07645A-2	Sequence 2, Appl1	1272	48.5	10.5	4550	1	US-08-804-227C-8	Sequence 8, Appl1
1200	48.5	10.5	132	4	PCT-US93-07645-2	Sequence 2, Appl1	1273	48.5	10.5	4550	1	US-08-804-227C-8	Sequence 8, Appl1
1201	48.5	10.5	136	2	US-09-378-238-33	Sequence 33, Appl1	1274	48.5	10.5	4550	1	US-08-804-227C-8	Sequence 8, Appl1
1202	48.5	10.5	136	2	US-09-626-896-29	Sequence 29, Appl1	1275	48.5	10.5	4550	1	US-08-804-227C-8	Sequence 8, Appl1
1203	48.5	10.5	136	2	US-09-841-730-29	Sequence 29, Appl1	1276	48.5	10.5	73	2	US-09-489-847-300	Sequence 300, App
1204	48.5	10.5	137	2	US-09-270-767-31876	Sequence 31876, A	1277	48.5	10.5	74	2	US-09-489-847-300	Sequence 229, App
1205	48.5	10.5	137	2	US-09-270-767-46893	Sequence 46893, A	1278	48.5	10.5	76	2	US-09-962-756-2182	Sequence 2182, App
1206	48.5	10.5	150	2	US-09-949-016-7926	Sequence 7926, Ap	1279	48.5	10.5	86	2	US-10-002-348A-186	Sequence 186, App
1207	48.5	10.5	157	2	US-09-378-238-31	Sequence 31, Appl1	1280	48.5	10.5	120	2	US-09-931-381A-12	Sequence 12, Appl1
1208	48.5	10.5	157	2	US-09-626-896-27	Sequence 27, Appl1	1281	48.5	10.5	120	2	US-09-513-998C-4290	Sequence 4290, Ap
1209	48.5	10.5	157	2	US-09-841-730-27	Sequence 27, Appl1	1282	48.5	10.5	120	2	US-09-898-753A-14	Sequence 14, Appl1
1210	48.5	10.5	198	2	US-09-489-039A-7760	Sequence 7760, Ap	1283	48.5	10.5	133	2	US-09-071-031-226	Sequence 226, App
1211	48.5	10.5	217	2	US-09-489-039A-30489	Sequence 30489, A	1284	48.5	10.5	133	2	US-09-071-031-226	Sequence 226, App
1212	48.5	10.5	217	2	US-09-489-039A-30489	Sequence 30489, A	1285	48.5	10.5	133	2	US-09-489-039A-30489	Sequence 30489, A
1213	48.5	10.5	247	1	US-07-885-089B-2	Sequence 2, Appl1	1286	48.5	10.5	136	2	US-09-270-767-31783	Sequence 31783, A
1214	48.5	10.5	247	1	US-07-885-089B-8	Sequence 8, Appl1	1287	48.5	10.5	136	2	US-09-270-767-31783	Sequence 31783, A
1215	48.5	10.5	256	2	US-09-198-452A-449	Sequence 449, App	1288	48.5	10.5	136	2	US-09-270-767-31783	Sequence 31783, A
1216	48.5	10.5	256	2	US-09-543-681A-4282	Sequence 4282, Ap	1289	48.5	10.5	142	2	US-09-621-976-460	Sequence 460, Ap
1217	48.5	10.5	257	2	US-09-438-185A-432	Sequence 432, App	1290	48.5	10.5	143	2	US-09-621-976-460	Sequence 460, Ap
1218	48.5	10.5	258	1	US-08-665-202-5	Sequence 5, Appl1	1291	48.5	10.5	143	2	US-09-621-976-460	Sequence 460, Ap
1219	48.5	10.5	258	2	US-09-315-574-5	Sequence 5, Appl1	1292	48.5	10.5	143	2	US-09-621-976-460	Sequence 460, Ap
1220	48.5	10.5	279	2	US-09-328-352-4717	Sequence 4717, Ap	1293	48.5	10.5	160	2	US-09-621-976-460	Sequence 460, Ap
1221	48.5	10.5	285	2	US-08-992-035A-1	Sequence 1, Appl1	1294	48.5	10.5	166	2	US-09-328-352-4665	Sequence 21952, A
1222	48.5	10.5	285	2	US-09-552-991A-33954	Sequence 33954, A	1295	48.5	10.5	170	2	US-09-489-039A-8313	Sequence 8313, Ap
1223	48.5	10.5	293	2	US-09-660-587-40	Sequence 40, Appl1	1296	48.5	10.5	180	2	US-09-270-767-35232	Sequence 40016, A
1224	48.5	10.5	293	2	US-09-314-701-44	Sequence 44, Appl1	1297	48.5	10.5	180	2	US-09-270-767-35232	Sequence 55232, A
1225	48.5	10.5	293	2	US-09-811-007A-40	Sequence 40, Appl1	1298	48.5	10.5	187	2	US-09-270-767-35232	Sequence 32761, A
1226	48.5	10.5	293	2	US-10-314-639-44	Sequence 44, Appl1	1299	48.5	10.5	192	2	US-09-475-316A-25	Sequence 25, Appl1
1227	48.5	10.5	293	2	US-10-059-964A-44	Sequence 44, Appl1	1300	48.5	10.5	192	2	US-09-475-316A-25	Sequence 25, Appl1
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ALIGNMENTS

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; Patent No. 6277574
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Klingner, Tod, M.
; APPLICANT: Azimzai, Yalda
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
; FILE REFERENCE: PB-0010 US
; CURRENT APPLICATION NUMBER: US/09/289,349
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
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; OTHER INFORMATION: 1900433CD1
US-09-289-349-11
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Best Local Similarity 100.0%; Pred. No. 2e-51;
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Getter, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Auelin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
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; PRIOR APPLICATION NUMBER: 60/049787
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 2e-51;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERYTALLLLAGITALEANDPPFANKDDPPYYDMKNIQLSGLTICGGLTLAGTIAVAATSGK 60
 Db 1 MERYTALLLLAGITALEANDPPFANKDDPPYYDMKNIQLSGLTICGGLTLAGTIAVAATSGK 60
 Qy 61 CKYSSOKHSPVEKAIPLITRESATTC 89
 Db 61 CKYSSOKHSPVEKAIPLITRESATTC 89

RESULT 3
 ; Sequence 262; Application US/09990444
 ; Patent No. 6930170
 ; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Auecin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/390,444
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-09
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RESULT 4
; Sequence 262, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deemeyer, Luc

;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gertsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C27
CURRENT APPLICATION NUMBER: US/09/997,333
CURRENT FILING DATE: 2001-11-15
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PRIOR APPLICATION NUMBER: 60/090862
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PRIOR APPLICATION NUMBER: 60/091544
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PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 2; Length 89;
Best local similarity 100.0%; Pred. No. 2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALILLAGLTALANDPANKDPEFYDMKNLQISGLICGLLAIAGIAVLGSK 60
DB 1 MERVTLALILLAGLTALANDPANKDPEFYDMKNLQISGLICGLLAIAGIAVLGSK 60
QY 61 CKYSSOKSHSPVPEKAIPLITPGSATTC 89
DB 61 CKYSSOKSHSPVPEKAIPLITPGSATTC 89

RESULT 5
Sequence 262, Application US/09992598
Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ahkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC20
CURRENT APPLICATION NUMBER: US/09/992,598
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088655
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/ PRIOR FILING DATE: 1998-07-02
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/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 2e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MERVTLALLLGLTALBANDPANKDDPFYDMKNLQSLICGGLAINGIAAVLSGK 60
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Db 1 MERVTLALLLGLTALBANDPANKDDPFYDMKNLQSLICGGLAINGIAAVLSGK 60
    |||||

Oy 61 CKYKSSQKQSHSPVEKAIPLITPGSATTG 89
    |||||
Db 61 CKYKSSQKQSHSPVEKAIPLITPGSATTG 89
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RESULT 6
US-09-724-864-58
/ Sequence 58, Application US/09724864
/ Patent No. 6380362
/ GENERAL INFORMATION:
/ APPLICANT: Watson, James D.
/ TITLE OF INVENTION: Polynucleotides, polypeptides expressed
/ FILE REFERENCE: 11000.1050U1
/ CURRENT APPLICATION NUMBER: US/09/724,864
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 4.0
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/ SEQ ID NO 58
/ LENGTH: 88
/ TYPE: PRT
/ ORGANISM: Mouse
US-09-724-864-58

Query Match          60.0%; Score 276.5; DB 2; Length 88;
Best Local Similarity 66.7%; Pred. No. 9e-28;
Matches 60; Conservative 8; Mismatches 19; Indels 3; Gaps 3;

Oy 1 MERVTLA-LLLIAGTALBANDPANKDDPFYDMKNLQSLICGGLAINGIAAVLSG 59
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Db 1 MEIRTCAPLLIAGLPALBANDP-VKDSPPFYDMESIQSLICGGLAINGIAAVLSG 59
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Oy 60 KCKYKSSQKQSHSPVEKAIPLITPGSATTG 89
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Db 60 KCKYKSSQKQSHSPVEKAIPLITPGSATTG 89
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RESULT 7
US-08-725-531-5
/ Sequence 5, Application US/08725531
/ Patent No. 5756310
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLIPID-LIKE PROTEIN
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: U.S.
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/725,531
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0128 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 87 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 951423
US-08-725-531-5

Query Match          55.6%; Score 256.5; DB 1; Length 87;
Best Local Similarity 61.5%; Pred. No. 3.2e-25;
Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;

Oy 1 MERVTLA-LLLIAGTALBANDPANKDDPFYDMKNLQSLICGGLAINGIAAVLSG 59
    |||||
Db 1 MEGITCAPLLIAGLPALBANDP-VKDSPPFYDMESIQSLICGGLAINGIAAVLSG 59
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Qy 60 KCKYSSQKQSP--VPEKAIPLITPGSATT 88
Db 60 KCK---CRNHTPSSLPEKVTPLITPGSAST 87

RESULT 8

US-08-738-127-5
Sequence 5, Application US/08738127
Patent No. 5919655
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Philip R.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738.127
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0141 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 951423
US-08-738-127-5

Query Match 55.6%; Score 256.5; DB 1; Length 87;
Best Local Similarity 61.5%; Pred. No. 3.2e-25;
Matches 56; Conservative 11; Mismatches 17; Indels 7; Gaps 4;

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Qy 60 KCKYSSQKQSP--VPEKAIPLITPGSATT 88
Db 60 KCK---CRNHTPSSLPEKVTPLITPGSAST 87

RESULT 9

US-09-213-392-5
Sequence 5, Application US/09213392
Patent No. 5943505
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213.392
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/083.661
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0128 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 951423
US-09-213-392-5

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Db 1 MEGITCALFLVLAGLPVLEANGP-VDKSPFYDWESLQSGMTFGGLICIAIAMLG 59
Qy 60 KCKYSSQKQSP--VPEKAIPLITPGSATT 88
Db 60 KCK---CRNHTPSSLPEKVTPLITPGSAST 87

RESULT 10

US-09-083-661-5
Sequence 5, Application US/09083661
Patent No. 5955283
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
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COMPUTER: IBM Compatible
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SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083.661

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
Db 60 KCKCKFGQKSGHH--PGETPPLITPGSA 85

RESULT 13
US-08-738-127-4
Sequence 4, Application US/08738127
Patent No. 5919655
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,127
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0141 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1085026
US-08-738-127-4

Query Match 46.5%; Score 214.5; DB 1; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.9e-20;
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;

Qy 1 MERVTLALL-LAGLTLEANDPFANKDPPFYDMKNQLSGSLTCGGLAIAAGIAVLG 59
Db 1 MQKVTGLGLVLAGFPVLDAND-LEDKNSPFYDMHSLQVGLICAGVLCAMGIITWSA 59

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
Db 60 KCKCKFGQKSGHH--PGETPPLITPGSA 85

RESULT 14
US-09-213-392-4
Sequence 4, Application US/09213392
Patent No. 5945505
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,392
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/083,661
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0128 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1085026
US-09-213-392-4

Query Match 46.5%; Score 214.5; DB 1; Length 87;
Best Local Similarity 54.5%; Pred. No. 7.9e-20;
Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;

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Db 1 MQKVTGLGLVLAGFPVLDAND-LEDKNSPFYDMHSLQVGLICAGVLCAMGIITWSA 59

Qy 60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
Db 60 KCKCKFGQKSGHH--PGETPPLITPGSA 85

RESULT 15
US-09-083-661-4
Sequence 4, Application US/09083661
Patent No. 5955283
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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(without alignments)
338.062 Million cell updates/sec

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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626	461	100.0	89	4	US-10-063-742-50 Sequence 50, Appl
741	461	100.0	89	5	US-10-972-317-50 Sequence 50, Appl
742	461	100.0	89	5	US-10-820-474A-35 Sequence 35, Appl
744	461	100.0	89	5	US-10-950-374-262 Sequence 262, App
747	374	81.1	186	4	US-10-295-027-210 Sequence 210, App
748	374	81.1	318	4	US-10-295-027-212 Sequence 212, App
749	276.5	60.0	88	3	US-09-866-050A-698 Sequence 698, App
750	214.5	46.5	87	4	US-10-176-847-24 Sequence 24, Appl
751	214.5	46.5	87	4	US-10-205-823-140 Sequence 140, App
752	214.5	46.5	87	4	US-10-177-293-166 Sequence 166, App
753	214.5	46.5	87	4	US-10-295-027-1358 Sequence 1358, App
754	214.5	46.5	87	6	US-11-051-454-140 Sequence 140, App
755	214.5	46.5	116	4	US-10-161-493-34 Sequence 34, Appl
756	209.5	45.4	86	4	US-10-161-493-32 Sequence 32, Appl
760	191.5	41.5	113	6	US-11-051-454-142 Sequence 142, App
761	191.5	41.5	113	6	US-11-051-454-142 Sequence 142, App
762	191.5	41.5	150	3	US-09-925-299-955 Sequence 955, App
763	129	28.0	92	3	US-09-981-876-238 Sequence 238, App
764	129	28.0	92	3	US-09-148-545-238 Sequence 238, App
765	129	28.0	92	3	US-09-803-190-120 Sequence 120, App
766	129	28.0	92	3	US-09-978-360A-776 Sequence 776, App
767	129	28.0	92	4	US-10-408-765A-1270 Sequence 1270, App
768	129	28.0	92	5	US-10-930-331-120 Sequence 120, App

769	129	28.0	92	5	US-10-979-111-238	Sequence 238, App
770	129	28.0	93	3	US-09-981-876-183	Sequence 183, App
771	129	28.0	93	3	US-09-148-545-183	Sequence 183, App
772	129	28.0	93	5	US-10-979-111-183	Sequence 183, App
773	121	26.2	70	3	US-09-981-876-269	Sequence 269, App
774	121	26.2	70	3	US-09-148-545-269	Sequence 269, App
775	121	26.2	70	5	US-10-979-111-269	Sequence 269, App
776	113.5	24.6	138	4	US-10-291-265-446	Sequence 446, App
777	112.5	24.4	95	4	US-10-291-265-918	Sequence 918, App
778	112.5	24.4	96	3	US-09-809-391-473	Sequence 473, App
779	112.5	24.4	96	3	US-09-882-171-473	Sequence 473, App
780	112.5	24.4	96	4	US-10-164-861-473	Sequence 473, App
807	112.5	24.4	120	3	US-09-997-428-199	Sequence 199, App
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1298	112.5	24.4	120	5	US-10-955-952-434	Sequence 434, App
1299	112.5	24.4	120	5	US-10-950-374-199	Sequence 199, App
1300	106	23.0	69	3	US-09-809-391-606	Sequence 606, App
1301	106	23.0	69	3	US-09-882-171-606	Sequence 606, App
1302	106	23.0	69	4	US-10-164-861-606	Sequence 606, App
1303	105.5	22.9	110	5	US-10-450-763-56705	Sequence 56705, A
1304	94	20.4	115	4	US-10-352-272-2	Sequence 2, Appl
1305	94	20.4	178	3	US-09-833-245-1532	Sequence 1532, App
1306	94	20.4	178	3	US-09-985-153-92	Sequence 92, Appl
1307	94	20.4	178	3	US-09-985-153-93	Sequence 93, Appl
1308	94	20.4	178	3	US-09-985-153-94	Sequence 94, Appl
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JOB time : 134 secs

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Prod. No. is the number of results predicted by chance to have a
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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	89	7	US-11-102-240-50 Sequence 50, Appl
2	214.5	46.5	87	6	US-10-821-234-1279 Sequence 1279, Ap
3	214.5	46.5	87	7	US-11-080-991-24 Sequence 24, Appl
4	113.5	24.6	138	7	US-11-000-463-446 Sequence 44, Appl
5	112.5	24.4	95	7	US-11-000-463-918 Sequence 918, Appl
7	94	20.4	178	6	US-10-821-234-1495 Sequence 1495, Ap
8	67.5	14.6	664	7	US-11-080-991-40 Sequence 40, Appl
9	61.5	13.3	977	7	US-11-093-274-39 Sequence 932, Ap
10	61	13.2	139	6	US-10-467-657-4932 Sequence 4932, Ap
11	59	12.8	858	6	US-10-613-744-6 Sequence 6, Appl
13	58.5	12.7	837	6	US-10-467-657-1464 Sequence 1464, Ap
14	57.5	12.5	324	6	US-10-858-730-113 Sequence 113, Appl
15	56.5	12.3	148	6	US-10-512-109-19 Sequence 19, Appl
16	55.5	12.0	384	7	US-11-108-185-14 Sequence 14, Appl
17	55.5	12.0	384	7	US-11-108-185-16 Sequence 16, Appl
18	55.5	12.0	384	7	US-11-108-185-18 Sequence 18, Appl
20	54.5	11.8	186	7	US-11-044-899-23 Sequence 23, Appl
21	54.5	11.8	384	7	US-11-108-185-2 Sequence 2, Appl
22	54.5	11.8	384	7	US-11-108-185-4 Sequence 4, Appl
23	54.5	11.8	895	7	US-11-150-406-2 Sequence 2, Appl
24	54.5	11.8	920	6	US-10-821-234-1159 Sequence 1129, Ap
25	54	11.7	346	7	US-11-186-284-189 Sequence 189, Appl
26	54	11.7	376	6	US-10-467-657-6138 Sequence 6138, Ap
27	53.5	11.6	244	7	US-11-186-284-97 Sequence 97, Appl
28	53.5	11.6	407	6	US-10-793-626-1578 Sequence 1578, Ap
30	53.5	11.6	495	6	US-10-613-744-5 Sequence 5, Appl

31	53	11.5	223	7	US-11-055-822-1130 Sequence 1130, Ap
32	53	11.5	267	6	US-10-995-561-552 Sequence 552, Appl
33	53	11.5	267	6	US-10-995-561-553 Sequence 553, Appl
34	52.5	11.4	384	7	US-11-108-185-6 Sequence 6, Appl
35	52.5	11.4	384	7	US-11-108-185-8 Sequence 8, Appl
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37	52.5	11.4	384	7	US-11-108-185-12 Sequence 12, Appl
38	52	11.3	112	7	US-11-000-463-282 Sequence 282, Appl
39	52	11.3	112	7	US-11-000-463-754 Sequence 754, Appl
40	52	11.3	378	7	US-11-082-389-404 Sequence 404, Appl
41	52	11.3	401	7	US-11-000-365-50 Sequence 50, Appl
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44	52	11.3	711	6	US-10-467-657-2966 Sequence 2966, Ap
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47	51.5	11.2	211	6	US-11-186-284-22 Sequence 22, Appl
48	51.5	11.2	244	6	US-10-510-386-110 Sequence 110, Appl
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50	51	11.1	265	6	US-10-467-657-5894 Sequence 5894, Appl
51	51	11.1	265	6	US-10-467-657-7494 Sequence 7494, Appl
52	51	11.1	280	7	US-11-143-980-34 Sequence 34, Appl
53	51	11.1	421	6	US-10-467-657-790 Sequence 790, Appl
54	51	11.1	774	7	US-11-000-463-439 Sequence 439, Appl
55	50.5	11.0	1211	7	US-11-186-284-4 Sequence 4, Appl
56	50	10.8	82	6	US-10-467-657-4684 Sequence 4684, Appl
57	50	10.8	334	6	US-10-467-657-2204 Sequence 2204, Appl
58	50	10.8	334	6	US-10-467-657-6504 Sequence 6504, Appl
59	50	10.8	346	7	US-11-000-365-52 Sequence 52, Appl
60	50	10.8	346	7	US-11-032-794-52 Sequence 52, Appl
61	50	10.8	390	6	US-10-793-626-1422 Sequence 1422, Appl
62	50	10.8	457	6	US-10-982-548-8 Sequence 8, Appl
63	50	10.8	457	6	US-10-982-548-13 Sequence 13, Appl
64	49.5	10.7	252	6	US-10-821-234-1445 Sequence 1445, Appl
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66	49.5	10.7	262	6	US-10-793-626-1568 Sequence 1568, Appl
67	49.5	10.7	394	6	US-10-793-626-3292 Sequence 3292, Appl
68	49.5	10.7	414	6	US-10-793-626-806 Sequence 806, Appl
69	49.5	10.7	557	7	US-11-191-375-4 Sequence 4, Appl
70	49.5	10.7	557	7	US-11-191-375-4 Sequence 4, Appl
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73	49	10.6	276	6	US-10-467-657-4158 Sequence 4158, Appl
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75	49	10.6	352	6	US-10-995-561-523 Sequence 523, Appl
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79	49	10.6	468	7	US-11-167-273-1 Sequence 1, Appl
80	49	10.6	529	6	US-10-821-234-1168 Sequence 1168, Appl
81	49	10.6	914	7	US-11-108-172-1066 Sequence 1066, Appl
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85	48.5	10.5	146	7	US-11-061-821-42 Sequence 42, Appl
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87	48.5	10.5	284	6	US-10-821-234-1280 Sequence 1280, Appl
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91	48.5	10.5	567	6	US-10-467-657-4328 Sequence 4328, Appl
92	48.5	10.5	615	6	US-10-982-545-14 Sequence 14, Appl
93	48.5	10.5	616	6	US-10-982-545-5 Sequence 5, Appl
94	48	10.4	68	6	US-10-467-657-4718 Sequence 4718, Appl
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96	48	10.4	407	7	US-11-092-140-4 Sequence 4, Appl
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98	48	10.4	840	6	US-10-645-441-1 Sequence 1, Appl
99	48	10.4	948	6	US-10-485-517-131 Sequence 131, Appl
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101	47.5	10.3	107	7	US-11-123-896-269 Sequence 269, Appl
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103	47.5	10.3	738	6	US-10-995-561-632 Sequence 632, Appl
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128	47	10.2	254	7	US-11-067-323-316	Sequence 316, App	201	46	10.0	330	6	US-10-846-172A-7	Sequence 7, Appli
129	47	10.2	254	7	US-11-067-323-326	Sequence 326, App	202	46	10.0	333	6	US-10-846-172A-6	Sequence 6, Appli
130	47	10.2	254	7	US-11-067-323-328	Sequence 328, App	203	46	10.0	377	6	US-10-821-234-1436	Sequence 1436, Ap
131	47	10.2	254	7	US-11-067-323-330	Sequence 330, App	204	46	10.0	407	6	US-11-051-267-515	Sequence 25, Appl
132	47	10.2	254	7	US-11-067-323-334	Sequence 334, App	205	46	10.0	421	6	US-10-793-626-1818	Sequence 1818, Ap
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145	47	10.2	489	6	US-10-858-730-198	Sequence 198, App	218	45.5	9.9	138	7	US-11-080-991-12	Sequence 12, Appl
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147	47	10.2	544	6	US-10-467-657-2436	Sequence 2436, Ap	220	45.5	9.9	202	6	US-10-858-730-86	Sequence 86, Appl
148	47	10.2	752	7	US-11-080-991-52	Sequence 52, Appl	221	45.5	9.9	254	7	US-11-067-323-450	Sequence 450, App
149	47	10.2	1006	6	US-10-467-657-8400	Sequence 8400, Ap	222	45.5	9.9	254	7	US-11-067-323-574	Sequence 574, App
150	47	10.2	1068	7	US-11-191-374-45	Sequence 45, Appl	223	45.5	9.9	269	6	US-10-995-561-535	Sequence 535, App
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159	46.5	10.1	328	6	US-11-083-389-4	Sequence 4, Appli	233	45.5	9.9	456	6	US-10-763-712A-66	Sequence 66, Appl
160	46.5	10.1	330	6	US-10-848-375-1	Sequence 1, Appli	234	45.5	9.9	502	6	US-10-763-712A-68	Sequence 68, Appl
161	46.5	10.1	330	6	US-11-184-380-12	Sequence 12, Appl	235	45.5	9.9	622	6	US-10-510-386-236	Sequence 236, App
162	46.5	10.1	342	6	US-10-689-742-218	Sequence 218, App	236	45.5	9.9	792	7	US-11-108-172-1127	Sequence 1127, Ap
163	46.5	10.1	374	7	US-11-051-267-20	Sequence 20, Appl	237	45.5	9.9	984	7	US-11-055-822-508	Sequence 508, App
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166	46.5	10.1	512	6	US-10-467-657-2284	Sequence 2284, Ap	240	45.5	9.9	1709	6	US-10-995-561-973	Sequence 973, App
167	46.5	10.1	512	6	US-10-467-657-6592	Sequence 6592, Ap	241	45	9.8	111	6	US-10-821-234-1547	Sequence 1547, Ap
168	46.5	10.1	522	7	US-11-055-822-1100	Sequence 1100, Ap	242	45	9.8	160	7	US-11-010-874-16	Sequence 16, Appl
169	46.5	10.1	550	7	US-11-184-380-14	Sequence 14, Appl	243	45	9.8	215	7	US-11-089-551A-15	Sequence 15, Appl
170	46.5	10.1	574	6	US-10-763-712A-6	Sequence 6, Appli	244	45	9.8	237	7	US-11-083-055-2	Sequence 2, Appli
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174	46.5	10.1	842	6	US-10-645-441-2	Sequence 2, Appli	248	45	9.8	310	7	US-11-025-834A-13	Sequence 13, Appl
175	46.5	10.1	1043	6	US-10-392-234A-34	Sequence 34, Appl	249	45	9.8	316	6	US-10-467-657-4414	Sequence 4414, Ap
176	46	10.0	58	6	US-10-613-744-28	Sequence 28, Appl	250	45	9.8	339	7	US-11-010-874-6	Sequence 6, Appli
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256	45	9.8	685	7	US-11-089-551A-3	Sequence 2, Appli	332	44	9.5	254	7	US-11-067-323-238	Sequence 238, App
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258	45	9.8	858	6	US-10-878-556A-36	Sequence 36, Appl	334	44	9.5	254	7	US-11-067-323-242	Sequence 242, App
259	45	9.8	903	7	US-11-057-058-65	Sequence 65, Appl	335	44	9.5	254	7	US-11-067-323-244	Sequence 244, App
260	45	9.8	1069	7	US-11-191-374-17	Sequence 17, Appl	336	44	9.5	254	7	US-11-067-323-246	Sequence 246, App
261	45	9.8	1069	7	US-11-191-375-17	Sequence 17, Appl	337	44	9.5	254	7	US-11-067-323-248	Sequence 248, App
262	45	9.8	1451	6	US-10-995-561-829	Sequence 829, App	338	44	9.5	254	7	US-11-067-323-250	Sequence 250, App
263	45	9.8	1458	6	US-11-096-274-2	Sequence 2, Appli	339	44	9.5	254	7	US-11-067-323-258	Sequence 258, App
264	44.5	9.7	98	6	US-10-467-657-6904	Sequence 6904, Ap	340	44	9.5	254	7	US-11-067-323-260	Sequence 260, App
265	44.5	9.7	124	6	US-10-467-657-3838	Sequence 3838, Ap	341	44	9.5	254	7	US-11-067-323-262	Sequence 262, App
266	44.5	9.7	148	6	US-10-512-109-21	Sequence 21, Appl	342	44	9.5	254	7	US-11-067-323-264	Sequence 264, App
267	44.5	9.7	165	6	US-10-467-657-6012	Sequence 6012, Ap	343	44	9.5	254	7	US-11-067-323-266	Sequence 266, App
268	44.5	9.7	186	7	US-11-044-899-21	Sequence 21, Appl	344	44	9.5	254	7	US-11-067-323-268	Sequence 268, App
269	44.5	9.7	186	7	US-11-044-899-22	Sequence 22, Appl	345	44	9.5	254	7	US-11-067-323-270	Sequence 270, App
270	44.5	9.7	190	6	US-10-467-657-2540	Sequence 2540, Ap	346	44	9.5	254	7	US-11-067-323-274	Sequence 274, App
271	44.5	9.7	198	7	US-11-082-389-302	Sequence 302, App	347	44	9.5	254	7	US-11-067-323-280	Sequence 280, App
272	44.5	9.7	244	6	US-10-793-626-566	Sequence 566, App	348	44	9.5	254	7	US-11-067-323-284	Sequence 284, App
273	44.5	9.7	255	6	US-10-510-386-66	Sequence 66, Appl	349	44	9.5	254	7	US-11-067-323-288	Sequence 288, App
274	44.5	9.7	255	6	US-10-510-386-156	Sequence 156, App	350	44	9.5	254	7	US-11-067-323-300	Sequence 300, App
275	44.5	9.7	281	7	US-11-082-389-304	Sequence 304, App	351	44	9.5	254	7	US-11-067-323-302	Sequence 302, App
276	44.5	9.7	304	6	US-10-467-657-7616	Sequence 7616, Ap	352	44	9.5	254	7	US-11-067-323-308	Sequence 308, App
278	44.5	9.7	310	7	US-11-025-834A-15	Sequence 15, Appl	353	44	9.5	254	7	US-11-067-323-310	Sequence 310, App
279	44.5	9.7	321	6	US-10-821-234-1192	Sequence 1192, Ap	354	44	9.5	254	7	US-11-067-323-312	Sequence 312, App
280	44.5	9.7	345	6	US-10-467-657-7598	Sequence 7598, Ap	355	44	9.5	254	7	US-11-067-323-314	Sequence 314, App
281	44.5	9.7	362	6	US-10-821-234-1148	Sequence 1148, Ap	356	44	9.5	254	7	US-11-067-323-318	Sequence 318, App
282	44.5	9.7	418	6	US-10-995-561-753	Sequence 753, App	357	44	9.5	254	7	US-11-067-323-324	Sequence 324, App
283	44.5	9.7	418	6	US-10-995-561-754	Sequence 754, App	358	44	9.5	254	7	US-11-067-323-334	Sequence 334, App
284	44.5	9.7	418	6	US-10-995-561-755	Sequence 755, App	359	44	9.5	254	7	US-11-067-323-338	Sequence 338, App
285	44.5	9.7	418	6	US-10-995-561-756	Sequence 756, App	360	44	9.5	254	7	US-11-067-323-348	Sequence 348, App
286	44.5	9.7	418	6	US-10-995-561-757	Sequence 757, App	361	44	9.5	254	7	US-11-067-323-350	Sequence 350, App
287	44.5	9.7	418	6	US-10-995-561-758	Sequence 758, App	362	44	9.5	254	7	US-11-067-323-356	Sequence 356, App
288	44.5	9.7	418	6	US-10-995-561-759	Sequence 759, App	363	44	9.5	254	7	US-11-067-323-360	Sequence 360, App
289	44.5	9.7	433	7	US-11-055-822-154	Sequence 154, App	364	44	9.5	254	7	US-11-067-323-366	Sequence 366, App
290	44.5	9.7	449	7	US-11-071-062-1	Sequence 1, Appli	365	44	9.5	254	7	US-11-067-323-368	Sequence 368, App
291	44.5	9.7	449	7	US-11-196-459-2	Sequence 2, Appli	366	44	9.5	254	7	US-11-067-323-384	Sequence 384, App
292	44.5	9.7	475	7	US-11-074-176-136	Sequence 136, App	367	44	9.5	254	7	US-11-067-323-388	Sequence 388, App
294	44.5	9.7	488	7	US-11-074-176-126	Sequence 126, App	368	44	9.5	254	7	US-11-067-323-392	Sequence 392, App
295	44.5	9.7	514	6	US-10-821-234-1511	Sequence 1511, Ap	369	44	9.5	254	7	US-11-067-323-394	Sequence 394, App
296	44.5	9.7	525	6	US-10-467-657-5462	Sequence 5462, Ap	370	44	9.5	254	7	US-11-067-323-396	Sequence 396, App
297	44.5	9.7	530	6	US-10-467-657-3804	Sequence 3804, Ap	371	44	9.5	254	7	US-11-067-323-398	Sequence 398, App
299	44.5	9.7	727	6	US-10-793-626-2862	Sequence 2862, Ap	372	44	9.5	254	7	US-11-067-323-402	Sequence 402, App
300	44.5	9.7	909	7	US-11-186-284-2	Sequence 2, Appli	373	44	9.5	254	7	US-11-067-323-404	Sequence 404, App
301	44.5	9.7	913	6	US-10-821-234-1040	Sequence 1040, Ap	374	44	9.5	254	7	US-11-067-323-408	Sequence 408, App
302	44.5	9.7	918	6	US-10-995-561-696	Sequence 696, App	375	44	9.5	254	7	US-11-067-323-410	Sequence 410, App
303	44.5	9.7	1065	7	US-11-191-374-16	Sequence 16, Appl	376	44	9.5	254	7	US-11-067-323-412	Sequence 412, App
304	44.5	9.7	1065	7	US-11-191-375-16	Sequence 16, Appl	377	44	9.5	254	7	US-11-067-323-414	Sequence 414, App
305	44.5	9.7	1167	6	US-10-601-368-18	Sequence 18, Appl	378	44	9.5	254	7	US-11-067-323-418	Sequence 418, App
306	44.5	9.7	1734	7	US-11-192-967-6	Sequence 6, Appli	379	44	9.5	254	7	US-11-067-323-420	Sequence 420, App
307	44.5	9.7	1734	7	US-11-193-715-6	Sequence 6, Appli	380	44	9.5	254	7	US-11-067-323-424	Sequence 424, App
308	44.5	9.7	2516	6	US-10-647-956A-2	Sequence 2, Appli	381	44	9.5	254	7	US-11-067-323-436	Sequence 436, App
309	44	9.5	129	6	US-10-967-527A-11	Sequence 11, Appl	382	44	9.5	254	7	US-11-067-323-444	Sequence 444, App
310	44	9.5	162	6	US-10-821-234-1343	Sequence 1343, Ap	383	44	9.5	254	7	US-11-067-323-544	Sequence 544, App
311	44	9.5	204	6	US-10-980-388-68	Sequence 68, Appl	384	44	9.5	254	7	US-11-067-323-552	Sequence 552, App
312	44	9.5	229	6	US-10-858-730-85	Sequence 85, Appl	385	44	9.5	254	7	US-11-067-323-584	Sequence 584, App
313	44	9.5	254	7	US-11-067-323-98	Sequence 98, Appl	386	44	9.5	254	7	US-11-067-323-594	Sequence 594, App
314	44	9.5	254	7	US-11-067-323-100	Sequence 100, App	387	44	9.5	254	7	US-11-067-323-602	Sequence 602, App
315	44	9.5	254	7	US-11-067-323-156	Sequence 156, App	388	44	9.5	254	7	US-11-067-323-612	Sequence 612, App
316	44	9.5	254	7	US-11-067-323-160	Sequence 160, App	389	44	9.5	254	7	US-11-067-323-732	Sequence 732, App
317	44	9.5	254	7	US-11-067-323-170	Sequence 170, App	390	44	9.5	262	6	US-10-467-657-7532	Sequence 7532, Ap
318	44	9.5	254	7	US-11-067-323-172	Sequence 172, App	391	44	9.5	274	6	US-10-467-657-1126	Sequence 1126, Ap
319	44	9.5	254	7	US-11-067-323-174	Sequence 174, App	392	44	9.5	307	6	US-10-467-657-6016	Sequence 6016, Ap
320	44	9.5	254	7	US-11-067-323-180	Sequence 180, App	393	44	9.5	325	6	US-10-467-657-11	Sequence 14, Appl
321	44	9.5	254	7	US-11-067-323-190	Sequence 190, App	394	44	9.5	325	6	US-10-467-657-5568	Sequence 5568, App
322	44	9.5	254	7	US-11-067-323-194	Sequence 194, App	395	44	9.5	333	6	US-10-949-720-33	Sequence 32, Appl
323	44	9.5	254	7	US-11-067-323-198	Sequence 198, App	396	44	9.5	355	6	US-10-967-527A-32	Sequence 32, Appl
324	44	9.5	254	7	US-11-067-323-200	Sequence 200, App	397	44	9.5	392	6	US-10-957-569-35	Sequence 35, Appl
325	44	9.5	254	7	US-11-067-323-202	Sequence 202, App	398	44	9.5	519	6	US-11-099-691-10	Sequence 10, Appl
326	44	9.5	254	7	US-11-067-323-204	Sequence 204, App	399	44	9.5	569	6	US-10-821-234-864	Sequence 864, App
327	44	9.5	254	7	US-11-067-323-208	Sequence 208, App	400	44	9.5	578	6	US-10-763-712A-34	Sequence 34, Appl
328	44	9.5	254	7	US-11-067-323-214	Sequence 214, App	401	44	9.5	610	6	US-10-858-730-292	Sequence 292, App

402	44	9.5	856	6	US-10-467-657-8534	Sequence 8534, Ap	475	43	9.3	254	7	US-11-067-323-256	Sequence 256, App
403	44	9.5	1730	7	US-11-192-967-4	Sequence 4, Appl1	476	43	9.3	254	7	US-11-067-323-290	Sequence 290, App
404	44	9.5	1730	7	US-11-193-715-4	Sequence 4, Appl1	477	43	9.3	254	7	US-11-067-323-322	Sequence 322, App
405	44	9.5	3689	7	US-11-075-185-4	Sequence 4, Appl1	478	43	9.3	254	7	US-11-067-323-340	Sequence 340, App
406	43.5	9.4	77	6	US-10-467-657-3770	Sequence 3770, Ap	479	43	9.3	254	7	US-11-067-323-346	Sequence 346, App
407	43.5	9.4	112	7	US-11-082-884-1	Sequence 1, Appl1	480	43	9.3	254	7	US-11-067-323-372	Sequence 372, App
408	43.5	9.4	132	6	US-10-465-561-22	Sequence 22, Appl1	481	43	9.3	254	7	US-11-067-323-382	Sequence 382, App
409	43.5	9.4	141	6	US-10-467-657-4110	Sequence 4110, Ap	482	43	9.3	254	7	US-11-067-323-386	Sequence 386, App
410	43.5	9.4	148	7	US-11-147-047-30	Sequence 30, Appl1	483	43	9.3	254	7	US-11-067-323-390	Sequence 390, App
411	43.5	9.4	159	7	US-11-147-047-29	Sequence 29, Appl1	484	43	9.3	254	7	US-11-067-323-390	Sequence 390, App
412	43.5	9.4	183	6	US-10-821-234-1485	Sequence 1485, Ap	485	43	9.3	254	7	US-11-067-323-368	Sequence 368, App
413	43.5	9.4	183	7	US-11-186-284-111	Sequence 111, App	486	43	9.3	254	7	US-11-067-323-378	Sequence 378, App
414	43.5	9.4	183	7	US-11-186-284-113	Sequence 113, App	487	43	9.3	254	7	US-11-067-323-610	Sequence 610, App
415	43.5	9.4	184	6	US-10-742-634-5	Sequence 5, Appl1	488	43	9.3	254	7	US-11-067-323-726	Sequence 726, App
416	43.5	9.4	184	6	US-10-967-527A-5	Sequence 5, Appl1	489	43	9.3	254	7	US-11-067-323-744	Sequence 744, App
417	43.5	9.4	250	7	US-11-054-515-1212	Sequence 1212, Ap	490	43	9.3	261	6	US-10-467-657-6154	Sequence 6154, Ap
418	43.5	9.4	254	7	US-11-067-323-88	Sequence 88, Appl1	491	43	9.3	280	6	US-10-858-730-200	Sequence 200, App
419	43.5	9.4	254	7	US-11-067-323-92	Sequence 92, Appl1	492	43	9.3	422	6	US-10-878-556A-172	Sequence 172, App
420	43.5	9.4	254	7	US-11-067-323-254	Sequence 254, App	493	43	9.3	445	7	US-11-112-882-29	Sequence 29, Appl1
421	43.5	9.4	257	7	US-11-054-515-1240	Sequence 1240, Ap	494	43	9.3	445	7	US-11-194-246-345	Sequence 345, App
422	43.5	9.4	266	6	US-10-884-730-114	Sequence 114, App	495	43	9.3	457	7	US-11-074-176-12	Sequence 12, Appl1
423	43.5	9.4	266	6	US-11-055-822-620	Sequence 620, App	496	43	9.3	502	7	US-11-021-441-7	Sequence 7, Appl1
424	43.5	9.4	276	7	US-11-062-186-40	Sequence 40, Appl1	497	43	9.3	563	7	US-11-021-441-9	Sequence 9, Appl1
425	43.5	9.4	292	6	US-10-510-386-74	Sequence 74, Appl1	498	43	9.3	574	7	US-11-021-441-15	Sequence 15, Appl1
426	43.5	9.4	309	6	US-10-858-730-364	Sequence 364, App	499	43	9.3	581	7	US-11-021-441-11	Sequence 11, Appl1
427	43.5	9.4	309	7	US-11-055-822-114	Sequence 114, App	500	43	9.3	581	7	US-10-821-334-1412	Sequence 1412, Ap
428	43.5	9.4	313	6	US-10-719-311-8	Sequence 8, Appl1	501	43	9.3	703	6	US-10-821-334-1412	Sequence 8476, Ap
429	43.5	9.4	334	6	US-11-055-822-980	Sequence 9852, App	502	43	9.3	718	6	US-10-467-657-8476	Sequence 25, Appl1
430	43.5	9.4	338	6	US-10-467-657-3852	Sequence 9, Appl1	503	43	9.3	737	6	US-10-878-556A-25	Sequence 46, Appl1
431	43.5	9.4	399	6	US-10-719-311-9	Sequence 1014, Ap	504	43	9.3	741	7	US-11-089-551A-46	Sequence 8, Appl1
432	43.5	9.4	407	6	US-10-995-361-1014	Sequence 368, App	505	43	9.3	856	6	US-10-510-947-8	Sequence 13, Appl1
433	43.5	9.4	412	6	US-10-793-626-368	Sequence 2, Appl1	506	43	9.3	856	6	US-11-042-988-13	Sequence 13, Appl1
434	43.5	9.4	432	7	US-11-014-361-2	Sequence 2, Appl1	507	43	9.3	886	6	US-10-821-334-1390	Sequence 1390, Ap
435	43.5	9.4	432	7	US-11-140-417-2	Sequence 2, Appl1	508	43	9.3	1035	7	US-11-021-441-4	Sequence 4, Appl1
436	43.5	9.4	438	7	US-11-140-417-2	Sequence 2908, Ap	509	43	9.3	2011	7	US-11-080-991-56	Sequence 56, Appl1
437	43.5	9.4	451	6	US-10-793-626-2908	Sequence 10, Appl1	510	43	9.3	3655	7	US-11-075-185-5	Sequence 5, Appl1
438	43.5	9.4	537	6	US-10-719-311-10	Sequence 169, App	511	43	9.3	7102	7	US-11-143-980-8	Sequence 48, Appl1
439	43.5	9.4	592	6	US-10-623-155-169	Sequence 26, Appl1	512	42.5	9.2	117	7	US-11-114-848-2	Sequence 2, Appl1
440	43.5	9.4	621	7	US-11-184-380-26	Sequence 67, Appl1	513	42.5	9.2	140	7	US-11-102-240-90	Sequence 90, Appl1
441	43.5	9.4	623	6	US-10-719-311-2	Sequence 11, Appl1	514	42.5	9.2	141	6	US-10-982-145-70	Sequence 70, Appl1
442	43.5	9.4	623	6	US-10-719-311-11	Sequence 47, Appl1	515	42.5	9.2	141	6	US-10-982-145-71	Sequence 71, Appl1
443	43.5	9.4	689	7	US-11-113-424-47	Sequence 86, Appl1	516	42.5	9.2	140	6	US-10-467-657-4330	Sequence 4330, Ap
444	43.5	9.4	750	6	US-10-688-742-86	Sequence 86, Appl1	517	42.5	9.2	154	7	US-11-055-822-894	Sequence 894, App
445	43.5	9.4	782	6	US-10-821-234-1592	Sequence 1592, Ap	518	42.5	9.2	167	6	US-10-821-234-1589	Sequence 1589, App
446	43.5	9.4	791	6	US-10-623-155-170	Sequence 679, App	519	42.5	9.2	225	6	US-10-793-626-1452	Sequence 1452, App
447	43.5	9.4	825	6	US-10-995-561-679	Sequence 5, Appl1	520	42.5	9.2	250	7	US-11-082-389-216	Sequence 216, App
448	43.5	9.4	852	7	US-11-104-923A-5	Sequence 410, App	521	42.5	9.2	266	7	US-11-102-240-2	Sequence 2, Appl1
449	43.5	9.4	881	6	US-10-623-155-430	Sequence 357, App	522	42.5	9.2	283	6	US-10-467-657-5210	Sequence 5210, Ap
450	43.5	9.4	920	6	US-10-623-155-357	Sequence 161, App	523	42.5	9.2	288	6	US-10-793-626-1118	Sequence 1118, App
451	43.5	9.4	943	6	US-10-623-155-161	Sequence 67, Appl1	524	42.5	9.2	329	6	US-10-858-730-108	Sequence 108, App
452	43.5	9.4	1032	6	US-10-392-234A-67	Sequence 63, Appl1	525	42.5	9.2	342	7	US-11-082-389-214	Sequence 214, App
453	43.5	9.4	1342	6	US-10-770-726-63	Sequence 12, Appl1	526	42.5	9.2	345	6	US-10-512-109-17	Sequence 17, Appl1
454	43.5	9.4	1342	7	US-11-113-202-12	Sequence 14, Appl1	527	42.5	9.2	346	7	US-11-077-386-24	Sequence 24, Appl1
455	43.5	9.4	1342	6	US-11-113-202-14	Sequence 7922, Ap	528	42.5	9.2	347	6	US-10-467-657-2962	Sequence 2962, Ap
456	43.5	9.4	1377	7	US-10-467-657-7922	Sequence 334, App	529	42.5	9.2	351	6	US-10-821-234-969	Sequence 969, App
457	43.5	9.4	1389	6	US-10-467-657-334	Sequence 1116, Ap	530	42.5	9.2	365	7	US-11-102-978-9	Sequence 9, Appl1
458	43.5	9.4	5405	6	US-11-108-172-1116	Sequence 29, Appl1	531	42.5	9.2	365	7	US-11-080-991-78	Sequence 78, Appl1
459	43	9.3	58	6	US-10-613-744-29	Sequence 99, Appl1	532	42.5	9.2	400	7	US-11-077-386-26	Sequence 26, Appl1
460	43	9.3	87	7	US-11-053-076-99	Sequence 466, App	533	42.5	9.2	450	7	US-11-087-100-20	Sequence 20, Appl1
461	43	9.3	91	7	US-11-123-896-466	Sequence 154, App	534	42.5	9.2	450	7	US-11-087-100-28	Sequence 28, Appl1
462	43	9.3	179	7	US-11-102-240-154	Sequence 43, Appl1	535	42.5	9.2	450	7	US-11-087-084-20	Sequence 20, Appl1
463	43	9.3	179	7	US-11-177-987-43	Sequence 27, Appl1	536	42.5	9.2	450	7	US-11-087-084-28	Sequence 28, Appl1
464	43	9.3	188	7	US-11-100-183-27	Sequence 18, Appl1	537	42.5	9.2	450	7	US-11-087-085-20	Sequence 20, Appl1
465	43	9.3	202	6	US-10-467-657-18	Sequence 5702, Ap	538	42.5	9.2	450	7	US-11-087-085-28	Sequence 28, Appl1
466	43	9.3	202	6	US-10-467-657-5702	Sequence 180, App	539	42.5	9.2	466	6	US-10-878-556A-31	Sequence 31, Appl1
467	43	9.3	216	6	US-10-485-517-180	Sequence 3362, Ap	540	42.5	9.2	468	6	US-10-467-657-776	Sequence 776, App
468	43	9.3	229	6	US-11-102-240-48	Sequence 8278, Ap	541	42.5	9.2	534	7	US-11-077-386-25	Sequence 25, Appl1
469	43	9.3	243	6	US-10-467-657-3362	Sequence 186, App	542	42.5	9.2	595	6	US-10-995-561-995	Sequence 95, App
470	43	9.3	244	6	US-10-467-657-8278	Sequence 212, App	543	42.5	9.2	631	6	US-10-995-561-546	Sequence 146, App
471	43	9.3	254	7	US-11-067-323-186	Sequence 222, App	544	42.5	9.2	668	7	US-11-113-424-112	Sequence 2098, App
472	43	9.3	254	7	US-11-067-323-212	Sequence 232, App	545	42.5	9.2	776	6	US-10-793-626-2098	Sequence 3, Appl1
473	43	9.3	254	7	US-11-067-323-224		547	42.5	9.2				
474	43	9.3	254	7	US-11-067-323-232		548	42.5	9.2	824	6	US-10-821-234-1008	Sequence 1008, App

549	42.5	9.2	1073	6	US-10-467-657-5230	Sequence 5230, Ap	623	41.5	9.0	181	6	US-10-467-657-6074	Sequence 6074, Ap
550	42.5	9.2	1124	7	US-11-195-197-9	Sequence 9, Appl	624	41.5	9.0	199	6	US-10-793-626-1342	Sequence 1342, Ap
551	42.5	9.2	1148	7	US-11-110-083-29	Sequence 29, Appl	625	41.5	9.0	199	6	US-10-995-561-902	Sequence 902, Ap
552	42.5	9.2	1149	7	US-11-110-083-30	Sequence 30, Appl	626	41.5	9.0	207	6	US-10-467-657-1944	Sequence 1944, Ap
553	42.5	9.2	1151	7	US-11-046-346-1	Sequence 1, Appl	627	41.5	9.0	216	6	US-11-082-389-32	Sequence 32, Appl
554	42.5	9.2	2059	7	US-11-087-100-4	Sequence 4, Appl	628	41.5	9.0	236	6	US-10-995-561-903	Sequence 903, Ap
555	42.5	9.2	2059	7	US-11-087-084-4	Sequence 4, Appl	629	41.5	9.0	251	6	US-10-793-626-3050	Sequence 3050, Ap
556	42.5	9.2	2059	7	US-11-087-085-4	Sequence 4, Appl	630	41.5	9.0	254	7	US-11-067-323-94	Sequence 94, Appl
557	42.5	9.2	3433	6	US-10-714-781A-67	Sequence 67, Appl	631	41.5	9.0	254	7	US-11-067-323-96	Sequence 96, Appl
558	42	9.1	166	6	US-10-467-657-1722	Sequence 1722, Ap	632	41.5	9.0	254	7	US-11-067-323-150	Sequence 150, Ap
559	42	9.1	166	7	US-11-194-246-418	Sequence 418, Ap	633	41.5	9.0	254	7	US-11-067-323-152	Sequence 152, Ap
560	42	9.1	205	6	US-10-821-234-968	Sequence 968, Ap	634	41.5	9.0	254	7	US-11-067-323-154	Sequence 154, Ap
561	42	9.1	219	6	US-10-793-626-966	Sequence 966, Ap	635	41.5	9.0	254	7	US-11-067-323-158	Sequence 158, Ap
562	42	9.1	237	7	US-11-074-176-178	Sequence 178, Ap	636	41.5	9.0	254	7	US-11-067-323-164	Sequence 164, Ap
563	42	9.1	254	7	US-11-067-323-428	Sequence 428, Ap	637	41.5	9.0	254	7	US-11-067-323-166	Sequence 166, Ap
564	42	9.1	254	7	US-11-067-323-480	Sequence 480, Ap	638	41.5	9.0	254	7	US-11-067-323-168	Sequence 168, Ap
565	42	9.1	254	7	US-11-067-323-482	Sequence 482, Ap	639	41.5	9.0	254	7	US-11-067-323-176	Sequence 176, Ap
566	42	9.1	254	7	US-11-067-323-484	Sequence 484, Ap	640	41.5	9.0	254	7	US-11-067-323-446	Sequence 446, Ap
567	42	9.1	254	7	US-11-067-323-486	Sequence 486, Ap	641	41.5	9.0	254	7	US-11-067-323-652	Sequence 652, Ap
568	42	9.1	254	7	US-11-067-323-488	Sequence 488, Ap	642	41.5	9.0	254	7	US-11-067-323-654	Sequence 654, Ap
569	42	9.1	254	7	US-11-067-323-548	Sequence 548, Ap	643	41.5	9.0	285	6	US-10-821-234-1304	Sequence 1304, Ap
570	42	9.1	254	7	US-11-067-323-558	Sequence 558, Ap	644	41.5	9.0	325	7	US-11-055-822-126	Sequence 126, Ap
571	42	9.1	254	7	US-11-067-323-564	Sequence 564, Ap	646	41.5	9.0	345	7	US-11-073-603-6	Sequence 6, Appl
572	42	9.1	254	7	US-11-067-323-628	Sequence 628, Ap	647	41.5	9.0	345	7	US-11-064-774A-149	Sequence 149, Ap
573	42	9.1	254	7	US-11-067-323-632	Sequence 632, Ap	648	41.5	9.0	353	6	US-10-793-626-634	Sequence 634, Ap
574	42	9.1	254	7	US-11-067-323-718	Sequence 718, Ap	649	41.5	9.0	378	6	US-10-995-561-891	Sequence 891, Ap
575	42	9.1	254	7	US-11-067-323-736	Sequence 736, Ap	650	41.5	9.0	392	6	US-10-793-626-194	Sequence 194, Ap
576	42	9.1	254	7	US-11-067-323-951	Sequence 951, Ap	651	41.5	9.0	394	7	US-11-074-176-310	Sequence 310, Ap
577	42	9.1	254	7	US-11-067-323-987	Sequence 987, Ap	652	41.5	9.0	408	6	US-10-467-657-2048	Sequence 2048, Ap
578	42	9.1	254	7	US-11-067-323-1003	Sequence 1003, Ap	653	41.5	9.0	414	6	US-11-074-176-46	Sequence 46, Appl
579	42	9.1	307	6	US-11-067-323-1079	Sequence 1079, Ap	654	41.5	9.0	419	6	US-10-821-234-1664	Sequence 1664, Ap
580	42	9.1	311	6	US-10-508-263-113	Sequence 113, Ap	655	41.5	9.0	462	7	US-11-105-864-8	Sequence 8, Appl
581	42	9.1	311	6	US-11-055-822-246	Sequence 246, Ap	656	41.5	9.0	468	7	US-11-055-822-68	Sequence 68, Appl
582	42	9.1	341	6	US-10-858-730-124	Sequence 124, Ap	658	41.5	9.0	513	7	US-11-102-240-124	Sequence 124, Ap
583	42	9.1	348	6	US-10-793-626-2866	Sequence 2866, Ap	659	41.5	9.0	528	6	US-10-858-730-88	Sequence 88, Appl
584	42	9.1	348	6	US-10-467-657-8350	Sequence 8350, Ap	660	41.5	9.0	528	6	US-10-467-657-1042	Sequence 1042, Ap
585	42	9.1	349	7	US-11-147-047-47	Sequence 47, Appl	662	41.5	9.0	574	6	US-10-763-712A-1	Sequence 1, Appl
586	42	9.1	351	6	US-11-067-884-4	Sequence 4, Appl	663	41.5	9.0	574	6	US-10-763-712A-102	Sequence 102, Ap
587	42	9.1	351	6	US-10-793-626-2040	Sequence 2040, Ap	664	41.5	9.0	647	7	US-11-080-991-32	Sequence 32, Appl
588	42	9.1	394	6	US-10-821-234-1194	Sequence 1194, Ap	665	41.5	9.0	657	7	US-11-080-991-48	Sequence 48, Appl
589	42	9.1	410	6	US-10-793-626-3258	Sequence 3258, Ap	666	41.5	9.0	745	6	US-11-110-082-37	Sequence 37, Appl
590	42	9.1	428	6	US-10-689-742-50	Sequence 50, Appl	667	41.5	9.0	745	6	US-10-858-730-224	Sequence 224, Ap
591	42	9.1	444	7	US-11-074-176-170	Sequence 170, Ap	668	41.5	9.0	745	7	US-11-055-822-226	Sequence 226, Ap
592	42	9.1	461	7	US-11-132-285-6	Sequence 6, Appl	669	41.5	9.0	745	7	US-11-055-822-714	Sequence 714, Ap
593	42	9.1	463	7	US-11-182-946-4	Sequence 4, Appl	670	41.5	9.0	745	7	US-11-055-822-756	Sequence 756, Ap
594	42	9.1	463	6	US-10-821-234-1094	Sequence 1094, Ap	671	41.5	9.0	745	7	US-11-168-476-2	Sequence 2, Appl
595	42	9.1	477	6	US-10-793-626-3250	Sequence 3250, Ap	672	41.5	9.0	772	7	US-11-147-238-2	Sequence 2, Appl
596	42	9.1	488	6	US-10-467-657-2362	Sequence 2362, Ap	673	41.5	9.0	772	7	US-11-147-238-5	Sequence 5, Appl
597	42	9.1	497	7	US-11-143-980-61	Sequence 61, Appl	674	41.5	9.0	787	6	US-10-467-657-2832	Sequence 2832, Ap
598	42	9.1	540	7	US-11-137-465-47	Sequence 47, Appl	675	41.5	9.0	887	6	US-10-467-657-3960	Sequence 3960, Ap
599	42	9.1	558	6	US-10-467-657-234	Sequence 234, Ap	676	41.5	9.0	904	6	US-10-967-664A-14	Sequence 14, Appl
600	42	9.1	550	6	US-10-467-657-924	Sequence 924, Ap	677	41.5	9.0	1018	7	US-11-067-121-17	Sequence 17, Appl
601	42	9.1	582	6	US-10-793-626-11080	Sequence 1080, Ap	678	41.5	9.0	1259	6	US-10-467-657-5510	Sequence 5510, Ap
602	42	9.1	601	6	US-10-995-561-993	Sequence 993, Ap	679	41.5	9.0	1709	7	US-11-135-885-35	Sequence 35, Appl
603	42	9.1	623	6	US-10-467-657-6260	Sequence 6260, Ap	680	41.5	9.0	1907	7	US-11-039-398-25	Sequence 25, Appl
604	42	9.1	623	6	US-10-995-561-996	Sequence 996, Ap	681	41.5	9.0	67	7	US-11-082-389-33	Sequence 33, Appl
605	42	9.1	686	6	US-10-821-234-1027	Sequence 1027, Ap	682	41.5	9.0	68	6	US-10-821-234-855	Sequence 855, Ap
606	42	9.1	688	6	US-10-821-234-1533	Sequence 1533, Ap	683	41.5	9.0	122	6	US-10-821-234-1538	Sequence 1538, Ap
607	42	9.1	716	6	US-10-467-657-6200	Sequence 6200, Ap	684	41.5	9.0	126	6	US-10-467-657-2240	Sequence 2240, Ap
608	42	9.1	744	6	US-10-467-657-1936	Sequence 1936, Ap	685	41.5	9.0	139	6	US-10-878-556A-117	Sequence 117, Ap
609	42	9.1	759	6	US-10-467-657-4186	Sequence 4186, Ap	686	41.5	9.0	154	7	US-11-082-544-14	Sequence 14, Appl
610	42	9.1	837	7	US-11-077-886-34	Sequence 34, Appl	687	41.5	9.0	161	6	US-10-821-234-1178	Sequence 1178, Ap
611	42	9.1	858	6	US-10-895-561-698	Sequence 698, Ap	688	41.5	9.0	166	6	US-10-793-626-1576	Sequence 1576, Ap
612	42	9.1	858	6	US-10-878-556A-113	Sequence 113, Ap	689	41.5	9.0	185	6	US-10-821-234-1198	Sequence 1198, Ap
613	42	9.1	1174	6	US-10-995-561-697	Sequence 997, Ap	690	41.5	9.0	185	6	US-10-529-118-2	Sequence 2, Appl
614	42	9.1	1356	6	US-10-995-561-904	Sequence 904, Ap	691	41.5	9.0	193	6	US-11-186-284-157	Sequence 157, Appl
615	42	9.1	1356	6	US-10-995-561-906	Sequence 906, Ap	692	41.5	9.0	193	7	US-11-186-284-159	Sequence 159, Ap
616	42	9.1	1503	7	US-11-087-100-6	Sequence 6, Appl	693	41.5	9.0	197	6	US-10-467-657-4944	Sequence 4944, Ap
617	42	9.1	1503	7	US-11-087-084-6	Sequence 6, Appl	694	41.5	9.0	209	6	US-10-793-626-1698	Sequence 1698, Ap
618	42	9.1	1503	7	US-11-087-085-6	Sequence 6, Appl	695	41.5	9.0	223	7	US-10-467-657-8494	Sequence 8494, Ap
619	42	9.1	74	6	US-10-467-657-4176	Sequence 4176, Ap	696	41.5	9.0	223	7	US-11-084-716-4	Sequence 4, Appl
620	42	9.1	81	6	US-10-821-234-1153	Sequence 1153, Ap	697	41.5	9.0	238	6	US-10-623-155-174	Sequence 174, Ap
621	41.5	9.0	115	6	US-10-793-626-1554	Sequence 1554, Ap	698	41.5	9.0	250	6	US-10-821-234-1542	Sequence 1542, Ap

699	41	8.9	250	7	US-11-054-515-1529	Sequence 1529, Ap	778	40.5	8.8	545	7	US-11-082-389-34	Sequence 34, Appl
700	41	8.9	252	7	US-11-054-515-1994	Sequence 1994, Ap	779	40.5	8.8	585	7	US-11-074-176-190	Sequence 190, Ap
701	41	8.9	252	7	US-11-054-515-2100	Sequence 2100, Ap	780	40.5	8.8	606	6	US-10-624-932-16	Sequence 16, Appl
702	41	8.9	254	7	US-11-054-515-1489	Sequence 1489, Ap	781	40.5	8.8	650	6	US-10-467-657-1948	Sequence 148, Ap
703	41	8.9	254	7	US-11-067-323-1033	Sequence 1081, Ap	782	40.5	8.8	662	7	US-11-030-439-8	Sequence 9, Appl1
704	41	8.9	254	7	US-11-067-323-1081	Sequence 1081, Ap	783	40.5	8.8	672	6	US-10-467-657-8280	Sequence 8280, Ap
705	41	8.9	264	7	US-11-188-743-24	Sequence 24, Appl	784	40.5	8.8	674	6	US-10-507-275-9	Sequence 9, Appl1
706	41	8.9	264	7	US-11-188-743-25	Sequence 25, Appl	785	40.5	8.8	698	6	US-10-995-561-939	Sequence 939, Ap
707	41	8.9	318	7	US-11-112-882-33	Sequence 32, Appl	787	40.5	8.8	725	6	US-10-995-561-938	Sequence 938, Ap
708	41	8.9	337	6	US-10-467-657-92	Sequence 97, Appl	788	40.5	8.8	773	6	US-10-995-561-852	Sequence 852, Ap
709	41	8.9	347	6	US-10-793-626-324	Sequence 324, App	789	40.5	8.8	817	6	US-10-793-626-50	Sequence 50, Appl
710	41	8.9	380	6	US-10-467-657-7258	Sequence 7258, Ap	790	40.5	8.8	817	6	US-10-793-626-1528	Sequence 1528, Ap
711	41	8.9	385	6	US-10-392-234A-22	Sequence 22, Appl	791	40.5	8.8	835	7	US-11-186-283-2	Sequence 2, Appl1
713	41	8.9	405	6	US-10-793-626-2152	Sequence 2152, Ap	792	40.5	8.8	858	6	US-10-995-561-854	Sequence 854, Ap
714	41	8.9	417	6	US-10-793-626-196	Sequence 196, App	793	40.5	8.8	892	6	US-10-507-275-3	Sequence 3, Appl1
715	41	8.9	417	6	US-10-793-626-950	Sequence 950, App	794	40.5	8.8	904	6	US-10-507-275-5	Sequence 5, Appl1
716	41	8.9	425	6	US-10-793-626-1012	Sequence 1012, Ap	795	40.5	8.8	904	7	US-11-087-227-12	Sequence 12, Appl
717	41	8.9	425	6	US-10-793-626-2434	Sequence 2434, Ap	796	40.5	8.8	919	7	US-11-102-440-10	Sequence 70, Appl
718	41	8.9	429	7	US-11-074-176-248	Sequence 248, App	797	40.5	8.8	1162	6	US-10-451-375-3	Sequence 3, Appl1
720	41	8.9	433	6	US-10-467-657-3294	Sequence 3294, Ap	798	40.5	8.8	1178	6	US-10-995-561-851	Sequence 851, Appl
721	41	8.9	457	7	US-10-467-657-7738	Sequence 7738, Ap	799	40.5	8.8	1210	7	US-11-191-374-10	Sequence 10, Appl
722	41	8.9	467	7	US-11-090-439-33	Sequence 33, Appl	800	40.5	8.8	1210	7	US-11-191-375-10	Sequence 10, Appl
723	41	8.9	476	6	US-10-878-556A-158	Sequence 158, App	801	40.5	8.8	1554	7	US-11-186-284-93	Sequence 93, Appl
725	41	8.9	522	7	US-11-080-991-104	Sequence 104, App	802	40.5	8.8	1841	7	US-11-057-058-6	Sequence 6, Appl
726	41	8.9	600	6	US-10-606-302-3	Sequence 3, Appl1	803	40.5	8.8	2261	6	US-10-995-561-600	Sequence 600, App
727	41	8.9	635	6	US-10-821-234-1673	Sequence 1673, Ap	804	40.5	8.8	4384	6	US-10-821-234-1120	Sequence 1120, Ap
729	41	8.9	720	7	US-11-113-424-28	Sequence 28, Appl	805	40.5	8.7	22	6	US-10-939-890-454	Sequence 454, App
730	41	8.9	747	7	US-11-113-424-26	Sequence 26, Appl	806	40	8.7	108	6	US-10-467-657-6202	Sequence 602, Ap
731	41	8.9	795	6	US-10-821-234-1675	Sequence 1675, Ap	807	40	8.7	108	7	US-11-082-389-278	Sequence 278, App
732	41	8.9	795	6	US-10-770-726-49	Sequence 49, Appl	808	40	8.7	117	7	US-11-000-463-295	Sequence 295, App
733	41	8.9	838	6	US-10-645-441-9	Sequence 9, Appl1	809	40	8.7	117	7	US-10-463-767	Sequence 767, App
734	41	8.9	1034	6	US-10-392-234A-30	Sequence 30, Appl	810	40	8.7	159	6	US-10-793-626-878	Sequence 878, App
736	41	8.9	1058	6	US-10-821-234-1473	Sequence 1473, Ap	811	40	8.7	171	6	US-10-793-626-2280	Sequence 2280, Ap
737	41	8.9	1058	6	US-10-878-556A-63	Sequence 63, Appl	812	40	8.7	195	6	US-10-467-657-8576	Sequence 8576, Ap
738	41	8.9	1058	7	US-11-069-642-105	Sequence 105, App	813	40	8.7	195	6	US-10-995-561-563	Sequence 563, App
739	41	8.9	1070	7	US-11/062	Sequence 4, Appl1	814	40	8.7	196	6	US-10-485-517-120	Sequence 120, App
740	41	8.9	1095	7	US-11/062	Sequence 7, Appl1	815	40	8.7	199	6	US-10-967-527A-4	Sequence 4, Appl1
741	41	8.9	1167	6	US-10-942-072-13	Sequence 13, Appl	816	40	8.7	207	6	US-10-467-657-2592	Sequence 2592, Ap
742	41	8.9	1168	6	US-10-942-072-11	Sequence 11, Appl	818	40	8.7	209	6	US-10-467-657-1099	Sequence 4090, Ap
743	41	8.9	118	7	US-11-000-463-274	Sequence 27, Appl	819	40	8.7	220	6	US-10-467-657-64	Sequence 64, Appl
744	40.5	8.8	118	7	US-11-000-463-746	Sequence 746, App	820	40	8.7	228	6	US-10-980-388-17	Sequence 17, Appl
745	40.5	8.8	118	7	US-10-793-626-2990	Sequence 2990, Ap	821	40	8.7	232	6	US-10-821-234-1199	Sequence 1199, Ap
746	40.5	8.8	135	6	US-10-467-657-5380	Sequence 5380, Ap	822	40	8.7	237	6	US-10-467-657-1794	Sequence 1794, Ap
747	40.5	8.8	182	6	US-10-467-657-4336	Sequence 4336, Ap	823	40	8.7	238	6	US-10-467-657-3602	Sequence 3602, Ap
748	40.5	8.8	205	7	US-11-055-822-1082	Sequence 1082, Ap	824	40	8.7	240	40	US-10-467-657-7868	Sequence 7868, Ap
749	40.5	8.8	219	7	US-10-467-657-6830	Sequence 6830, Ap	825	40	8.7	246	6	US-10-467-657-3824	Sequence 3824, Ap
750	40.5	8.8	223	6	US-10-467-657-1576	Sequence 1576, Ap	826	40	8.7	247	7	US-11-000-463-399	Sequence 399, App
751	40.5	8.8	225	6	US-11-170-653-24	Sequence 24, Appl	827	40	8.7	252	7	US-11-034-515-1575	Sequence 1575, Ap
752	40.5	8.8	225	7	US-10-467-657-1246	Sequence 1246, Ap	828	40	8.7	254	7	US-11-067-323-62	Sequence 62, Appl
753	40.5	8.8	251	7	US-11-054-515-1837	Sequence 1837, Ap	829	40	8.7	254	7	US-11-067-323-64	Sequence 64, Appl
754	40.5	8.8	251	7	US-10-995-561-601	Sequence 601, App	830	40	8.7	254	7	US-11-067-323-56	Sequence 56, Appl
755	40.5	8.8	252	6	US-11-067-323-162	Sequence 162, App	831	40	8.7	254	7	US-11-067-323-676	Sequence 676, App
756	40.5	8.8	254	7	US-11-067-323-538	Sequence 538, App	832	40	8.7	254	7	US-11-067-323-306	Sequence 306, App
757	40.5	8.8	254	7	US-10-467-657-116	Sequence 116, App	833	40	8.7	254	7	US-11-067-323-536	Sequence 536, App
758	40.5	8.8	257	6	US-10-467-657-3698	Sequence 3698, Ap	834	40	8.7	254	7	US-11-067-323-586	Sequence 586, App
759	40.5	8.8	301	6	US-10-467-657-7356	Sequence 7356, Ap	835	40	8.7	254	7	US-11-067-323-676	Sequence 676, App
760	40.5	8.8	302	6	US-10-793-626-1144	Sequence 1144, Ap	836	40	8.7	254	7	US-11-067-323-676	Sequence 676, App
761	40.5	8.8	310	6	US-10-485-517-409	Sequence 409, App	837	40	8.7	254	7	US-11-137-465-34	Sequence 34, Appl
762	40.5	8.8	317	7	US-11-129-143-67	Sequence 67, Appl	838	40	8.7	256	7	US-11-000-463-871	Sequence 871, App
764	40.5	8.8	338	7	US-11-074-176-42	Sequence 42, Appl	839	40	8.7	256	7	US-11-055-822-550	Sequence 550, App
765	40.5	8.8	363	6	US-10-995-561-602	Sequence 602, App	840	40	8.7	264	7	US-11-055-822-596	Sequence 596, App
766	40.5	8.8	393	6	US-10-467-657-1038	Sequence 1038, Ap	841	40	8.7	280	6	US-10-689-742-160	Sequence 160, App
767	40.5	8.8	408	7	US-11-140-417-6	Sequence 6, Appl1	843	40	8.7	292	7	US-11-069-642-117	Sequence 117, App
768	40.5	8.8	423	7	US-11-184-156-2	Sequence 2, Appl1	844	40	8.7	322	6	US-10-508-263-52	Sequence 52, Appl
769	40.5	8.8	478	6	US-10-689-742-184	Sequence 184, App	846	40	8.7	326	6	US-10-793-626-3238	Sequence 338, Ap
770	40.5	8.8	482	6	US-10-633-150-14	Sequence 14, Appl	847	40	8.7	333	7	US-11-082-389-402	Sequence 402, App
771	40.5	8.8	482	7	US-11-073-457-14	Sequence 14, Appl	848	40	8.7	337	6	US-10-467-657-1674	Sequence 4674, Ap
772	40.5	8.8	504	7	US-11-073-460-14	Sequence 14, Appl	849	40	8.7	338	7	US-11-055-822-584	Sequence 584, App
773	40.5	8.8	504	6	US-10-878-556A-126	Sequence 126, App	850	40	8.7	359	7	US-11-012-762-12	Sequence 12, Appl
774	40.5	8.8	512	6	US-10-467-657-2772	Sequence 2772, Ap	851	40	8.7	370	6	US-10-821-234-1021	Sequence 1021, Ap
775	40.5	8.8	525	7	US-11-082-389-36	Sequence 36, Appl	852	40	8.7	370	6	US-10-821-234-1105	Sequence 1105, Ap
776	40.5	8.8	542	7	US-11-153-747-6	Sequence 6, Appl1	853	40	8.7	370	6	US-10-467-657-7966	Sequence 7966, Ap
777	40.5	8.8	542	7	US-11-153-747-6	Sequence 6, Appl1	854	40	8.7	394	6	US-10-467-657-7966	Sequence 7966, Ap

855	40	8.7	408	6	US-10-793-626-2286	Sequence 2286, Ap	930	39.5	8.6	254	7	US-11-067-323-12	Sequence 12, Appl
856	40	8.7	409	6	US-10-793-626-2002	Sequence 2002, Ap	931	39.5	8.6	254	7	US-11-067-323-14	Sequence 14, Appl
857	40	8.7	409	6	US-10-793-626-2306	Sequence 2306, Ap	932	39.5	8.6	254	7	US-11-067-323-15	Sequence 16, Appl
858	40	8.7	422	7	US-11-080-248-4	Sequence 4, Appl1	933	39.5	8.6	254	7	US-11-067-323-20	Sequence 20, Appl
859	40	8.7	424	6	US-10-485-517-405	Sequence 405, App	934	39.5	8.6	254	7	US-11-067-323-22	Sequence 22, Appl
860	40	8.7	455	6	US-10-847-867-28	Sequence 28, Appl	935	39.5	8.6	254	7	US-11-067-323-24	Sequence 24, Appl
861	40	8.7	455	6	US-10-847-867-30	Sequence 30, Appl	936	39.5	8.6	254	7	US-11-067-323-26	Sequence 26, Appl
862	40	8.7	455	6	US-10-847-867-31	Sequence 31, Appl	937	39.5	8.6	254	7	US-11-067-323-30	Sequence 30, Appl
863	40	8.7	455	6	US-10-847-867-32	Sequence 32, Appl	938	39.5	8.6	254	7	US-11-067-323-32	Sequence 32, Appl
864	40	8.7	455	6	US-10-847-867-33	Sequence 33, Appl	939	39.5	8.6	254	7	US-11-067-323-34	Sequence 34, Appl
865	40	8.7	455	6	US-10-847-867-34	Sequence 34, Appl	940	39.5	8.6	254	7	US-11-067-323-36	Sequence 36, Appl
866	40	8.7	466	6	US-10-467-657-2360	Sequence 2360, Ap	941	39.5	8.6	254	7	US-11-067-323-40	Sequence 40, Appl
867	40	8.7	479	6	US-10-821-234-871	Sequence 871, App	942	39.5	8.6	254	7	US-11-067-323-42	Sequence 42, Appl
868	40	8.7	494	6	US-10-467-657-4376	Sequence 4376, Ap	943	39.5	8.6	254	7	US-11-067-323-46	Sequence 46, Appl
869	40	8.7	500	6	US-10-821-234-1458	Sequence 1458, Ap	944	39.5	8.6	254	7	US-11-067-323-48	Sequence 48, Appl
871	40	8.7	541	7	US-11-000-463-238	Sequence 238, App	945	39.5	8.6	254	7	US-11-067-323-50	Sequence 50, Appl
872	40	8.7	592	6	US-10-467-657-350	Sequence 550, App	946	39.5	8.6	254	7	US-11-067-323-52	Sequence 52, Appl
873	40	8.7	604	6	US-10-942-072-4	Sequence 4, Appl1	947	39.5	8.6	254	7	US-11-067-323-54	Sequence 54, Appl
874	40	8.7	667	6	US-10-821-234-1477	Sequence 1477, Ap	948	39.5	8.6	254	7	US-11-067-323-56	Sequence 56, Appl
875	40	8.7	692	7	US-11-045-802-26	Sequence 26, Appl	949	39.5	8.6	254	7	US-11-067-323-58	Sequence 58, Appl
876	40	8.7	730	7	US-11-082-389-358	Sequence 358, App	950	39.5	8.6	254	7	US-11-067-323-60	Sequence 60, Appl
877	40	8.7	737	6	US-10-878-556A-99	Sequence 99, Appl	951	39.5	8.6	254	7	US-11-067-323-68	Sequence 68, Appl
878	40	8.7	757	7	US-11-110-082-35	Sequence 35, Appl	952	39.5	8.6	254	7	US-11-067-323-70	Sequence 70, Appl
879	40	8.7	761	7	US-11-110-082-34	Sequence 34, Appl	953	39.5	8.6	254	7	US-11-067-323-72	Sequence 72, Appl
880	40	8.7	802	6	US-10-510-386-2	Sequence 2, Appl1	954	39.5	8.6	254	7	US-11-067-323-74	Sequence 74, Appl
881	40	8.7	805	6	US-10-485-517-198	Sequence 198, App	955	39.5	8.6	254	7	US-11-067-323-76	Sequence 76, Appl
882	40	8.7	829	6	US-10-512-109-27	Sequence 27, Appl	956	39.5	8.6	254	7	US-11-067-323-78	Sequence 78, Appl
883	40	8.7	874	7	US-11-012-762-8	Sequence 8, Appl1	957	39.5	8.6	254	7	US-11-067-323-80	Sequence 80, Appl
884	40	8.7	882	7	US-11-012-762-34	Sequence 34, Appl	958	39.5	8.6	254	7	US-11-067-323-82	Sequence 82, Appl
886	40	8.7	1015	6	US-10-467-657-180	Sequence 180, App	959	39.5	8.6	254	7	US-11-067-323-84	Sequence 84, Appl
887	40	8.7	1015	6	US-10-467-657-3764	Sequence 3764, Ap	960	39.5	8.6	254	7	US-11-067-323-86	Sequence 86, Appl
888	40	8.7	1029	6	US-10-821-234-908	Sequence 908, App	961	39.5	8.6	254	7	US-11-067-323-90	Sequence 90, Appl
889	40	8.7	1121	7	US-11-113-751-24	Sequence 24, Appl	962	39.5	8.6	254	7	US-11-067-323-102	Sequence 102, App
890	40	8.7	1159	7	US-11-113-751-27	Sequence 27, Appl	963	39.5	8.6	254	7	US-11-067-323-114	Sequence 114, App
891	40	8.7	1167	6	US-10-942-072-6	Sequence 6, Appl1	964	39.5	8.6	254	7	US-11-067-323-112	Sequence 112, App
892	40	8.7	1236	7	US-11-080-991-108	Sequence 68, Appl	965	39.5	8.6	254	7	US-11-067-323-114	Sequence 114, App
893	40	8.7	1306	6	US-10-995-561-1027	Sequence 1027, Ap	966	39.5	8.6	254	7	US-11-067-323-118	Sequence 118, App
894	40	8.7	1463	6	US-10-971-982-3	Sequence 3, Appl1	967	39.5	8.6	254	7	US-11-067-323-120	Sequence 120, App
895	40	8.7	1717	7	US-11-192-967-2	Sequence 2, Appl1	968	39.5	8.6	254	7	US-11-067-323-122	Sequence 122, App
896	40	8.7	1717	7	US-11-193-715-2	Sequence 2, Appl1	969	39.5	8.6	254	7	US-11-067-323-124	Sequence 124, App
897	40	8.7	2047	7	US-11-013-759-4	Sequence 4, Appl1	970	39.5	8.6	254	7	US-11-067-323-126	Sequence 126, App
898	40	8.7	2047	7	US-11-013-759-7	Sequence 7, Appl1	971	39.5	8.6	254	7	US-11-067-323-128	Sequence 128, App
899	40	8.7	3623	6	US-10-995-561-593	Sequence 593, App	972	39.5	8.6	254	7	US-11-067-323-130	Sequence 130, App
900	39.5	8.6	72	7	US-11-053-076-316	Sequence 316, App	973	39.5	8.6	254	7	US-11-067-323-132	Sequence 132, App
901	39.5	8.6	82	6	US-10-467-657-5456	Sequence 5456, Ap	974	39.5	8.6	254	7	US-11-067-323-134	Sequence 134, App
902	39.5	8.6	89	6	US-10-999-866-27	Sequence 27, Appl	975	39.5	8.6	254	7	US-11-067-323-136	Sequence 136, App
903	39.5	8.6	89	7	US-11-061-821-27	Sequence 27, Appl	976	39.5	8.6	254	7	US-11-067-323-138	Sequence 138, App
904	39.5	8.6	91	7	US-11-074-176-352	Sequence 352, App	977	39.5	8.6	254	7	US-11-067-323-140	Sequence 140, App
905	39.5	8.6	95	7	US-11-074-176-180	Sequence 180, App	978	39.5	8.6	254	7	US-11-067-323-142	Sequence 142, App
906	39.5	8.6	111	6	US-10-793-626-730	Sequence 730, App	979	39.5	8.6	254	7	US-11-067-323-144	Sequence 144, App
907	39.5	8.6	113	6	US-10-467-657-1872	Sequence 1872, Ap	980	39.5	8.6	254	7	US-11-067-323-146	Sequence 146, App
908	39.5	8.6	139	6	US-10-793-626-2992	Sequence 2992, Ap	981	39.5	8.6	254	7	US-11-067-323-148	Sequence 148, App
909	39.5	8.6	157	6	US-10-793-626-3268	Sequence 3268, Ap	982	39.5	8.6	254	7	US-11-067-323-228	Sequence 228, App
910	39.5	8.6	173	6	US-10-467-657-772	Sequence 772, App	983	39.5	8.6	254	7	US-11-067-323-422	Sequence 422, App
911	39.5	8.6	211	6	US-10-858-730-102	Sequence 102, App	984	39.5	8.6	254	7	US-11-067-323-426	Sequence 426, App
912	39.5	8.6	214	6	US-10-467-657-5302	Sequence 5302, Ap	985	39.5	8.6	254	7	US-11-067-323-440	Sequence 440, App
913	39.5	8.6	221	6	US-10-467-657-3194	Sequence 3194, Ap	986	39.5	8.6	254	7	US-11-067-323-448	Sequence 448, App
914	39.5	8.6	223	6	US-11-112-882-88	Sequence 88, Appl	987	39.5	8.6	254	7	US-11-067-323-452	Sequence 452, App
915	39.5	8.6	225	6	US-10-467-657-5214	Sequence 5214, Ap	988	39.5	8.6	254	7	US-11-067-323-454	Sequence 454, App
916	39.5	8.6	230	6	US-10-510-386-198	Sequence 198, App	989	39.5	8.6	254	7	US-11-067-323-456	Sequence 456, App
917	39.5	8.6	230	7	US-11-080-628-24	Sequence 24, Appl	990	39.5	8.6	254	7	US-11-067-323-458	Sequence 458, App
918	39.5	8.6	236	7	US-11-000-463-390	Sequence 390, App	991	39.5	8.6	254	7	US-11-067-323-470	Sequence 470, App
919	39.5	8.6	246	6	US-10-793-626-162	Sequence 162, App	992	39.5	8.6	254	7	US-11-067-323-472	Sequence 472, App
920	39.5	8.6	246	6	US-10-878-556A-194	Sequence 194, App	993	39.5	8.6	254	7	US-11-067-323-476	Sequence 476, App
921	39.5	8.6	252	6	US-10-821-234-1193	Sequence 1193, Ap	994	39.5	8.6	254	7	US-11-067-323-480	Sequence 480, App
922	39.5	8.6	252	7	US-11-067-323-18	Sequence 18, Appl	995	39.5	8.6	254	7	US-11-067-323-492	Sequence 492, App
923	39.5	8.6	252	7	US-11-067-323-28	Sequence 28, Appl	996	39.5	8.6	254	7	US-11-067-323-494	Sequence 494, App
924	39.5	8.6	253	6	US-10-821-234-1438	Sequence 1438, Ap	997	39.5	8.6	254	7	US-11-067-323-500	Sequence 500, App
925	39.5	8.6	254	7	US-11-067-323-2	Sequence 2, Appl1	998	39.5	8.6	254	7	US-11-067-323-502	Sequence 502, App
926	39.5	8.6	254	7	US-11-067-323-4	Sequence 4, Appl1	999	39.5	8.6	254	7	US-11-067-323-508	Sequence 508, App
927	39.5	8.6	254	7	US-11-067-323-6	Sequence 6, Appl1	1000	39.5	8.6	254	7	US-11-067-323-512	Sequence 512, App
928	39.5	8.6	254	7	US-11-067-323-8	Sequence 8, Appl1	1001	39.5	8.6	254	7	US-11-067-323-514	Sequence 514, App
929	39.5	8.6	254	7	US-11-067-323-10	Sequence 10, Appl	1002	39.5	8.6	254	7	US-11-067-323-516	Sequence 516, App

1003	39.5	8.6	254	7	US-11-067-323-528	Sequence 528, App	1076	39.5	8.6	404	6	US-10-793-626-1204	Sequence 1204, Ap
1004	39.5	8.6	254	7	US-11-067-323-530	Sequence 530, App	1077	39.5	8.6	410	6	US-10-858-730-233	Sequence 233, App
1005	39.5	8.6	254	7	US-11-067-323-532	Sequence 532, App	1078	39.5	8.6	413	7	US-11-060-029-4	Sequence 4, Appl1
1006	39.5	8.6	254	7	US-11-067-323-534	Sequence 534, App	1079	39.5	8.6	445	7	US-11-000-463-461	Sequence 461, App
1007	39.5	8.6	254	7	US-11-067-323-552	Sequence 552, App	1080	39.5	8.6	465	6	US-10-793-626-2928	Sequence 2228, Ap
1008	39.5	8.6	254	7	US-11-067-323-554	Sequence 554, App	1081	39.5	8.6	478	7	US-11-054-385-8	Sequence 8, Appl1
1009	39.5	8.6	254	7	US-11-067-323-556	Sequence 556, App	1082	39.5	8.6	499	6	US-10-467-657-7096	Sequence 2096, Ap
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1011	39.5	8.6	254	7	US-11-067-323-570	Sequence 570, App	1084	39.5	8.6	528	6	US-10-858-730-89	Sequence 89, Appl1
1012	39.5	8.6	254	7	US-11-067-323-572	Sequence 572, App	1085	39.5	8.6	544	6	US-10-485-517-253	Sequence 253, App
1013	39.5	8.6	254	7	US-11-067-323-576	Sequence 576, App	1086	39.5	8.6	564	6	US-10-485-517-290	Sequence 290, App
1014	39.5	8.6	254	7	US-11-067-323-578	Sequence 578, App	1087	39.5	8.6	587	6	US-10-925-970-6	Sequence 6, Appl1
1015	39.5	8.6	254	7	US-11-067-323-580	Sequence 580, App	1088	39.5	8.6	648	6	US-10-467-657-7802	Sequence 2802, Ap
1016	39.5	8.6	254	7	US-11-067-323-582	Sequence 582, App	1089	39.5	8.6	686	7	US-11-113-424-46	Sequence 46, Appl1
1017	39.5	8.6	254	7	US-11-067-323-584	Sequence 584, App	1090	39.5	8.6	695	7	US-11-029-003-8	Sequence 8, Appl1
1018	39.5	8.6	254	7	US-11-067-323-598	Sequence 598, App	1091	39.5	8.6	753	6	US-10-858-730-225	Sequence 225, App
1019	39.5	8.6	254	7	US-11-067-323-620	Sequence 620, App	1092	39.5	8.6	794	6	US-10-793-626-1050	Sequence 1050, Ap
1020	39.5	8.6	254	7	US-11-067-323-622	Sequence 622, App	1093	39.5	8.6	822	6	US-10-645-441-15	Sequence 15, Appl1
1021	39.5	8.6	254	7	US-11-067-323-624	Sequence 624, App	1094	39.5	8.6	858	6	US-10-645-441-18	Sequence 18, Appl1
1022	39.5	8.6	254	7	US-11-067-323-640	Sequence 640, App	1095	39.5	8.6	858	6	US-10-645-441-20	Sequence 20, Appl1
1023	39.5	8.6	254	7	US-11-067-323-642	Sequence 642, App	1096	39.5	8.6	858	6	US-10-645-441-23	Sequence 23, Appl1
1024	39.5	8.6	254	7	US-11-067-323-644	Sequence 644, App	1097	39.5	8.6	859	7	US-11-000-463-423	Sequence 423, App
1025	39.5	8.6	254	7	US-11-067-323-646	Sequence 646, App	1098	39.5	8.6	859	7	US-11-000-463-895	Sequence 895, App
1026	39.5	8.6	254	7	US-11-067-323-648	Sequence 648, App	1099	39.5	8.6	898	7	US-11-174-150-43	Sequence 43, Appl1
1027	39.5	8.6	254	7	US-11-067-323-650	Sequence 650, App	1100	39.5	8.6	914	6	US-10-467-657-638	Sequence 638, App
1028	39.5	8.6	254	7	US-11-067-323-684	Sequence 684, App	1101	39.5	8.6	1049	6	US-10-392-234A-12	Sequence 12, Appl1
1029	39.5	8.6	254	7	US-11-067-323-686	Sequence 686, App	1102	39.5	8.6	1115	7	US-11-113-751-46	Sequence 46, Appl1
1030	39.5	8.6	254	7	US-11-067-323-688	Sequence 688, App	1103	39.5	8.6	1127	6	US-10-858-730-13	Sequence 13, Appl1
1031	39.5	8.6	254	7	US-11-067-323-690	Sequence 690, App	1104	39.5	8.6	1133	7	US-11-113-751-48	Sequence 48, Appl1
1032	39.5	8.6	254	7	US-11-067-323-692	Sequence 692, App	1105	39.5	8.6	1198	6	US-10-451-375-4	Sequence 4, Appl1
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1034	39.5	8.6	254	7	US-11-067-323-696	Sequence 696, App	1107	39.5	8.6	2004	6	US-10-467-657-84	Sequence 84, Appl1
1035	39.5	8.6	254	7	US-11-067-323-698	Sequence 698, App	1108	39.5	8.6	2004	6	US-10-467-657-6322	Sequence 6322, App
1036	39.5	8.6	254	7	US-11-067-323-700	Sequence 700, App	1109	39.5	8.6	3073	7	US-11-143-980-50	Sequence 50, Appl1
1037	39.5	8.6	254	7	US-11-067-323-704	Sequence 704, App	1110	39.5	8.6	3690	6	US-10-995-561-1016	Sequence 1016, Ap
1038	39.5	8.6	254	7	US-11-067-323-706	Sequence 706, App	1111	39.5	8.6	3714	6	US-10-925-561-1015	Sequence 1015, Ap
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1040	39.5	8.6	254	7	US-11-067-323-710	Sequence 710, App	1113	39	8.5	43	6	US-10-957-8878-222	Sequence 1276, Ap
1041	39.5	8.6	254	7	US-11-067-323-712	Sequence 712, App	1114	39	8.5	78	6	US-10-467-657-1276	Sequence 3, Appl1
1042	39.5	8.6	254	7	US-11-067-323-714	Sequence 714, App	1115	39	8.5	83	7	US-11-179-844-3	Sequence 748, App
1043	39.5	8.6	254	7	US-11-067-323-716	Sequence 716, App	1116	39	8.5	86	7	US-11-055-822-3	Sequence 52, Appl1
1044	39.5	8.6	254	7	US-11-067-323-720	Sequence 720, App	1117	39	8.5	90	7	US-11-053-076-52	Sequence 5070, App
1045	39.5	8.6	254	7	US-11-067-323-722	Sequence 722, App	1118	39	8.5	98	7	US-11-084-554-220	Sequence 520, App
1046	39.5	8.6	254	7	US-11-067-323-728	Sequence 728, App	1119	39	8.5	104	6	US-10-467-657-5070	Sequence 5070, Ap
1047	39.5	8.6	254	7	US-11-067-323-740	Sequence 740, App	1120	39	8.5	105	7	US-11-179-844-1	Sequence 1, Appl1
1048	39.5	8.6	254	7	US-11-067-323-742	Sequence 742, App	1121	39	8.5	104	7	US-11-040-114-2	Sequence 2, Appl1
1049	39.5	8.6	266	6	US-10-884-730-345	Sequence 345, App	1122	39	8.5	108	7	US-11-074-176-144	Sequence 144, App
1050	39.5	8.6	273	6	US-10-793-626-728	Sequence 728, App	1123	39	8.5	122	7	US-11-092-140-30	Sequence 30, Appl1
1051	39.5	8.6	273	6	US-10-467-657-7792	Sequence 7792, App	1124	39	8.5	129	6	US-10-485-517-178	Sequence 178, App
1052	39.5	8.6	280	6	US-10-967-457-75	Sequence 75, Appl1	1125	39	8.5	131	7	US-11-062-186-65	Sequence 6530, Ap
1053	39.5	8.6	296	6	US-10-467-657-3198	Sequence 3198, Ap	1126	39	8.5	132	6	US-10-467-657-6430	Sequence 6430, Ap
1054	39.5	8.6	304	7	US-11-055-822-108	Sequence 108, App	1127	39	8.5	139	7	US-11-082-389-294	Sequence 294, App
1055	39.5	8.6	319	7	US-11-184-005-8	Sequence 8, Appl1	1128	39	8.5	154	7	US-11-082-544-12	Sequence 12, Appl1
1056	39.5	8.6	322	6	US-10-467-657-3484	Sequence 3484, Ap	1129	39	8.5	156	7	US-11-055-822-744	Sequence 744, App
1057	39.5	8.6	334	6	US-10-858-730-114	Sequence 114, App	1130	39	8.5	162	6	US-10-467-657-7062	Sequence 7062, Ap
1058	39.5	8.6	338	6	US-10-821-234-1565	Sequence 1565, App	1131	39	8.5	184	7	US-11-084-591-5	Sequence 5, Appl1
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1063	39.5	8.6	367	6	US-10-793-626-1202	Sequence 1202, Ap	1136	39	8.5	207	6	US-10-858-730-196	Sequence 196, App
1064	39.5	8.6	369	6	US-10-432-483-18	Sequence 18, Appl1	1137	39	8.5	224	6	US-10-467-657-5378	Sequence 5378, Ap
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1164	39	8.5	254	7	US-11-067-323-510	Sequence 510, App	1237	39	8.5	254	7	US-11-067-323-874	Sequence 874, App
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1335	39	8.5	254	7	US-11-067-323-1115	Sequence 1115, Ap	1335	39	8.5	1048	6	US-10-392-234A-20	Sequence 20, Appl
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1338	39	8.5	254	7	US-11-067-323-1121	Sequence 1121, Ap	1338	39	8.5	1081	7	US-11-113-751-38	Sequence 38, Appl
1339	39	8.5	254	7	US-11-067-323-1123	Sequence 1123, Ap	1339	39	8.5	1083	7	US-11-113-751-42	Sequence 42, Appl
1340	39	8.5	254	7	US-11-067-323-1125	Sequence 1125, Ap	1340	39	8.5	1084	7	US-11-113-751-40	Sequence 40, Appl
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1345	39	8.5	254	7	US-11-067-323-1135	Sequence 1135, Ap	1345	39	8.5	1116	7	US-11-113-751-42	Sequence 42, Appl
1346	39	8.5	254	7	US-11-067-323-1137	Sequence 1137, Ap	1346	39	8.5	1121	7	US-11-113-751-19	Sequence 19, Appl
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1348	39	8.5	254	7	US-11-067-323-1141	Sequence 1141, Ap	1348	39	8.5	1152	7	US-11-113-751-26	Sequence 36, Appl
1349	39	8.5	254	7	US-11-067-323-1143	Sequence 1143, Ap	1349	39	8.5	1152	7	US-11-080-026-4	Sequence 4, Appl
1350	39	8.5	255	7	US-11-054-515-1539	Sequence 1153, Ap	1350	39	8.5	1153	7	US-11-113-751-64	Sequence 44, Appl
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1352	39	8.5	255	7	US-11-067-323-1019	Sequence 1019, Ap	1352	39	8.5	1188	6	US-10-601-368-21	Sequence 21, Appl
1353	39	8.5	258	7	US-11-054-515-1841	Sequence 1841, Ap	1353	39	8.5	1199	6	US-10-821-234-1126	Sequence 1126, Appl
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1356	39	8.5	294	6	US-10-467-657-2876	Sequence 2876, Ap	1356	39	8.5	1308	7	US-11-113-202-16	Sequence 16, Appl
1357	39	8.5	305	6	US-10-467-657-8482	Sequence 8482, Ap	1357	39	8.5	1365	6	US-10-995-561-867	Sequence 867, Appl
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1359	39	8.5	308	6	US-10-995-561-944	Sequence 944, Appl	1359	39	8.5	1435	6	US-10-995-561-869	Sequence 869, Appl
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1362	39	8.5	329	6	US-10-510-386-36	Sequence 36, Appl	1362	39	8.5	1438	7	US-10-985-205-3	Sequence 3, Appl
1363	39	8.5	330	6	US-10-510-386-196	Sequence 196, Appl	1363	39	8.5	1439	7	US-11-085-771-2	Sequence 2, Appl
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1365	39	8.5	343	6	US-10-467-657-7256	Sequence 7256, Appl	1365	39	8.5	1441	7	US-10-467-657-8698	Sequence 8698, Appl
1366	39	8.5	348	6	US-10-467-657-4840	Sequence 4840, Appl	1366	39	8.5	1442	7	US-11-053-076-156	Sequence 156, Appl
1367	39	8.5	357	7	US-11-108-528-60	Sequence 60, Appl	1367	39	8.5	1443	7	US-11-000-463-934	Sequence 934, Appl

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1445	38.5	8.4	101	6	US-10-510-386-170	Sequence 170, App
1447	38.5	8.4	118	7	US-11-000-463-462	Sequence 462, App
1448	38.5	8.4	126	6	US-10-467-657-8468	Sequence 8468, App
1449	38.5	8.4	137	6	US-10-793-626-104	Sequence 104, App
1450	38.5	8.4	140	7	US-11-118-855-11	Sequence 11, Appl
1451	38.5	8.4	146	6	US-10-467-657-4204	Sequence 4204, App
1452	38.5	8.4	188	6	US-10-793-626-152	Sequence 152, App
1453	38.5	8.4	223	7	US-11-084-716-2	Sequence 2, Appl
1456	38.5	8.4	232	7	US-11-170-653-64	Sequence 64, Appl
1457	38.5	8.4	235	7	US-11-194-246-407	Sequence 407, App
1458	38.5	8.4	237	6	US-10-884-730-336	Sequence 336, App
1459	38.5	8.4	237	7	US-11-082-389-240	Sequence 240, App
1460	38.5	8.4	250	7	US-11-054-515-1280	Sequence 1280, App
1461	38.5	8.4	254	7	US-11-067-323-116	Sequence 116, App
1462	38.5	8.4	259	7	US-11-054-515-1270	Sequence 1270, App
1463	38.5	8.4	266	6	US-10-884-730-334	Sequence 334, App
1464	38.5	8.4	279	6	US-10-467-657-8266	Sequence 8266, App
1465	38.5	8.4	288	6	US-10-793-626-2914	Sequence 2914, App
1466	38.5	8.4	295	6	US-10-793-626-2998	Sequence 2998, App
1467	38.5	8.4	301	6	US-10-858-730-126	Sequence 126, App
1468	38.5	8.4	301	7	US-11-055-822-56	Sequence 56, Appl
1469	38.5	8.4	313	6	US-10-793-626-2892	Sequence 2892, App
1470	38.5	8.4	313	6	US-10-793-626-3146	Sequence 3146, App
1471	38.5	8.4	316	6	US-10-510-386-244	Sequence 244, App
1473	38.5	8.4	353	7	US-11-096-850-2	Sequence 2, Appl
1474	38.5	8.4	357	6	US-10-467-657-2500	Sequence 2500, App
1475	38.5	8.4	357	6	US-10-467-657-6648	Sequence 6648, App
1476	38.5	8.4	357	7	US-11-055-822-734	Sequence 734, App
1477	38.5	8.4	365	7	US-11-082-389-236	Sequence 236, App
1478	38.5	8.4	376	7	US-11-075-185-15	Sequence 15, Appl
1479	38.5	8.4	397	7	US-11-060-008-8	Sequence 8, Appl
1480	38.5	8.4	402	6	US-10-858-730-30	Sequence 30, Appl
1481	38.5	8.4	402	7	US-11-055-822-778	Sequence 778, App
1482	38.5	8.4	402	7	US-11-055-822-780	Sequence 780, App
1483	38.5	8.4	403	6	US-10-485-517-165	Sequence 165, Appl
1484	38.5	8.4	413	7	US-11-060-008-9	Sequence 9, Appl
1485	38.5	8.4	419	6	US-10-821-234-1556	Sequence 1556, App
1486	38.5	8.4	431	6	US-10-821-234-1065	Sequence 1065, App
1487	38.5	8.4	431	6	US-10-467-657-202	Sequence 202, App
1488	38.5	8.4	434	6	US-10-467-657-6310	Sequence 6310, App
1489	38.5	8.4	434	6	US-10-793-626-2222	Sequence 2222, App
1490	38.5	8.4	449	7	US-11-196-459-1	Sequence 1, Appl
1491	38.5	8.4	452	6	US-10-467-657-3312	Sequence 3312, App
1492	38.5	8.4	462	6	US-10-763-712A-60	Sequence 60, Appl
1493	38.5	8.4	462	6	US-10-763-712A-62	Sequence 62, Appl
1494	38.5	8.4	465	6	US-10-467-657-1292	Sequence 1292, App
1495	38.5	8.4	471	6	US-10-995-561-901	Sequence 901, App
1496	38.5	8.4	480	7	US-11-074-176-2	Sequence 2, Appl
1497	38.5	8.4	485	6	US-10-467-657-946	Sequence 946, App
1498	38.5	8.4	505	6	US-10-467-657-6228	Sequence 6228, App
1499	38.5	8.4	513	6	US-10-793-626-2954	Sequence 2954, App
1500	38.5	8.4	513	6	US-10-650-326B-16	Sequence 16, Appl

Search completed: December 14, 2005, 06:36:43
Job time : 11 secs

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103	58	12.6	185	2	AG1054	probable exported
104	58	12.6	196	2	E75612	hypothetical prote
105	58	12.6	215	2	AF0650	probable membrane
106	58	12.6	257	2	A64459	diphthine synthase
107	58	12.6	277	2	S44252	raffinose operon r
108	58	12.6	368	2	T26425	hypothetical prote
109	58	12.6	376	2	AH1795	hypothetical membr
110	58	12.6	398	2	A82081	cell division prot
111	58	12.6	462	2	F75588	probable kynurenin
112	58	12.6	4836	2	T14346	herc2 protein - mo
113	57.5	12.5	71	2	D23876	vitelllogenin B2 pr
114	57.5	12.5	139	2	AF0685	hypothetical prote
115	57.5	12.5	324	2	T36805	conserved hypotnet
116	57.5	12.5	342	2	A47673	photosystem II chl
117	57.5	12.5	356	2	C72475	hypothetical prote
118	57.5	12.5	374	2	T10415	virus envelope pro
119	57.5	12.5	461	2	B83601	probable transport
120	57.5	12.5	461	2	AF0579	C4-dicarboxylate a
121	57.5	12.5	523	2	B83629	probable ATP-bindi
122	57.5	12.5	528	2	I84205	potassium channel
123	57.5	12.5	594	2	B90586	transpurt protein
124	57.5	12.5	636	2	S47299	gene F protein - r
125	57.5	12.5	662	2	T44034	hypothetical prote
126	57.5	12.5	662	2	T44034	hypothetical prote
127	57.5	12.5	1902	1	B44858	lactocepin (EC 3.4
128	57	12.4	148	2	C84690	probable membrane
129	57	12.4	258	2	JN0766	adenomedullin pre
130	57	12.4	269	2	F71251	probable uridine p
131	57	12.4	269	2	AG2268	hypothetical prote
132	57	12.4	342	2	A30189	iron stress-induce
133	57	12.4	374	2	T05660	hypothetical prote
134	57	12.4	385	2	T04725	nodulin-like prote
135	57	12.4	440	2	H86312	hypothetical prote
136	57	12.4	456	2	H96902	F2H15.2 protein -
137	57	12.4	457	2	B64769	membrane protein,
138	57	12.4	457	2	B64769	proline permease t
139	57	12.4	457	2	D90685	proline permease t
140	57	12.4	457	2	H85535	c4-dicarboxylate a
141	57	12.4	461	2	D90711	danc protein - Bac
142	57	12.4	461	2	C64796	transport of dicar
143	57	12.4	461	2	H85561	photoystem II 44k
144	57	12.4	487	2	S73277	homeotic protein R
145	56.5	12.3	114	2	E43559	21k protein - Shlg
146	56.5	12.3	187	2	S70186	probable exported
147	56.5	12.3	233	2	AD0905	probable lipoprote
148	56.5	12.3	233	2	F70668	uridine phosphoryl
149	56.5	12.3	258	2	D84336	potassium channel
150	56.5	12.3	361	2	S19552	endothelapepsin (EC
151	56.5	12.3	419	2	S42136	hypothetical prote
152	56.5	12.3	471	2	T04911	potassium uptake p
153	56.5	12.3	485	2	B97506	spOVb related memb
154	56.5	12.3	500	2	F97025	Na+/H+ antiporter
155	56.5	12.3	614	2	A69845	conserved hypotnet
156	56.5	12.3	670	1	E70040	glycoprotein H pre
157	56.5	12.3	686	1	VBEBPA	glycoprotein H
158	56.5	12.3	686	1	VBEBPA	glycoprotein H - s
159	56.5	12.3	686	2	S15478	hypothetical prote
160	56.5	12.3	852	2	S25359	hypothetical prote
161	56	12.1	79	1	TREPVK	K+ channel blocker
162	56	12.1	196	2	E64231	hypothetical prote
163	56	12.1	222	2	F82353	conserved hypotnet
164	56	12.1	261	2	AB2966	conserved hypotnet
165	56	12.1	261	2	B98317	ATP synthase chain
166	56	12.1	388	2	T09885	hypothetical prote
167	56	12.1	411	2	C87586	metal ion efflux m
168	56	12.1	436	2	G70058	hypothetical prote
169	56	12.1	440	2	C97376	probable transpore
170	56	12.1	440	2	A12593	MPS permease (limp
171	56	12.1	449	2	H70546	hypothetical prote
172	56	12.1	503	2	S36514	LI protein - human
173	56	12.1	547	2	D95337	probable manganese
174	56	12.1	558	2	S29125	dimethylalliline mo
175	56	12.1	578	2	B37852	phosphotransferase
176	56	12.1	594	2	A83096	probable permease
177	56	12.1	626	2	D70178	PTS system, fructo
178	56	12.1	736	2	C69451	cationic amino aci
179	56	12.1	1118	2	C95385	probable adenylate
180	56	12.1	1305	2	AB0168	probable cell divi
181	56	12.1	2055	2	T30259	multiple PDZ domai
182	56	12.1	3329	2	T42205	breat cancer susc
183	56	12.1	5170	2	T15348	hypothetical prote
184	55.5	12.0	245	2	A90521	hypothetical prote
185	55.5	12.0	249	4	T44821	bacteriorhodopsin
186	55.5	12.0	254	2	E75496	conserved hypotnet
187	55.5	12.0	256	2	E75496	hypothetical prote
188	55.5	12.0	259	4	T44820	bacteriorhodopsin
189	55.5	12.0	262	1	RAHSB	bacteriorhodopsin
190	55.5	12.0	262	2	H84300	bacteriorhodopsin
191	55.5	12.0	270	2	B82934	pancreatic elastas
192	55.5	12.0	299	2	B82943	hypothetical prote
193	55.5	12.0	309	2	C95138	legatose-6-phospha
194	55.5	12.0	309	2	A98006	hypothetical prote
195	55.5	12.0	316	2	G75388	exoz protein - Rhi
196	55.5	12.0	317	2	S16299	acetyltransferase
197	55.5	12.0	317	2	B95975	photosystem II chl
198	55.5	12.0	344	2	S42648	photosystem II chl
199	55.5	12.0	344	2	AB2306	photosystem II chl
200	55.5	12.0	346	2	C71042	probable chreonine
201	55.5	12.0	376	2	F72868	occlusion-derived
202	55.5	12.0	383	2	S53379	probable membrane
203	55.5	12.0	385	2	F86464	hypothetical prote
204	55.5	12.0	389	2	B81347	probable aspartate
205	55.5	12.0	456	2	T22347	hypothetical prote
206	55.5	12.0	459	2	D86669	amino acid permeas
207	55.5	12.0	545	2	A12337	hypothetical prote
208	55.5	12.0	609	2	S28283	hypothetical prote
209	55.5	12.0	625	2	S13919	potassium channel
210	55.5	12.0	648	2	C71658	probable primosoma
211	55.5	12.0	716	2	T03695	delta 1 pyrraline-
212	55.5	12.0	851	2	T12503	hypothetical prote
213	55.5	12.0	946	1	A29550	methyltetrahydrr
214	55.5	12.0	1217	2	T22672	hypothetical prote
215	55.5	12.0	1423	2	A49206	exo-beta-D-fructos
216	55.5	12.0	2054	2	T46652	multi PDZ domain p
217	55	11.9	52	2	T32956	hypothetical prote
218	55	11.9	52	2	T33694	hypothetical prote
219	55	11.9	128	2	F71371	hypothetical prote
220	55	11.9	169	2	S18653	hypothetical prote
221	55	11.9	212	2	E82135	conserved hypotnet
222	55	11.9	268	2	S05471	embryonic abundant
223	55	11.9	268	2	S14068	seed protein precu
224	55	11.9	288	2	T12462	hypothetical prote
225	55	11.9	312	2	B75405	endopeptidase-rela
226	55	11.9	334	2	S54438	hemin permease (va
227	55	11.9	336	2	AH0201	probable zinc-bind
228	55	11.9	340	2	AP2896	hypothetical prote
229	55	11.9	340	2	H97671	hypothetical prote
230	55	11.9	344	2	E84043	glyceraledehyde-3-p
231	55	11.9	357	2	A23641	R2 protein, testis
232	55	11.9	376	1	S17246	choirimate synthas
233	55	11.9	404	2	S34031	KRR3 protein - Yea
234	55	11.9	410	2	AH2895	hypothetical prote
235	55	11.9	410	2	C97671	hypothetical prote
236	55	11.9	443	2	B86180	probable maltose-b
237	55	11.9	459	2	A87201	protein Y1G11.3 (I
238	55	11.9	461	2	S57713	conserved hypotnet
239	55	11.9	482	1	F2K4C	probable mannosyl
240	55	11.9	482	2	AG1147	photosystem II chl
241	55	11.9	484	2	A41467	F60 extracellular
242	55	11.9	654	2	A96235	protein F60 precu
243	55	11.9	654	2	AC3051	hydroxamate-depend
244	55	11.9	716	2	E69672	hypothetical prote
245	55	11.9	2531	2	A18188	penicillin-binding
246	55	11.9	2531	2	A46019	notch protein homo
247	54.5	11.8	173	2	S33295	notch-1 protein -
248	54.5	11.8	177	2	G75285	translocon-associa
						hypothetical prote

249	54.5	11.8	185	2	T51844	RING-H2 finger pro	322	54	11.7	909	2	T00009	probable primase (
250	54.5	11.8	204	2	AC1961	ATP-dependent Clp	323	54	11.7	967	2	I40889	sarcosine oxidase
251	54.5	11.8	226	2	S76020	endopeptidase Clp	324	54	11.7	993	2	A38437	probable homeotic
252	54.5	11.8	255	2	F86203	hypothetical prote	325	54	11.7	1072	2	T50949	veprolin related
253	54.5	11.8	269	2	T19947	hypothetical prote	326	54	11.7	1222	2	G72614	probable reverse g
254	54.5	11.8	276	2	AC1838	hypothetical prote	327	54	11.7	1283	2	T18939	hypothetical prote
255	54.5	11.8	282	2	PQ0376	cell fusion glycop	328	53.5	11.6	114	2	C90344	hypothetical prote
256	54.5	11.8	296	2	F83145	probable epoxide h	329	53.5	11.6	153	3	T49895	oleosin-like prote
257	54.5	11.8	296	2	A85698	transposase for IS	330	53.5	11.6	173	2	G01145	hypothetical prote
258	54.5	11.8	296	2	A99840	transposase for IS	331	53.5	11.6	211	2	G82573	CDP-diacylglycerol
259	54.5	11.8	304	2	S59965	phosphotransferase	332	53.5	11.6	225	1	CYRGE	epsilon-crystallin
260	54.5	11.8	337	2	G87487	conserved hypothet	333	53.5	11.6	269	2	D96957	uncharacterized me
261	54.5	11.8	362	2	S77244	biotin synthase (E	334	53.5	11.6	346	2	D70558	cell fusion glycop
262	54.5	11.8	369	2	E83122	hypothetical prote	335	53.5	11.6	296	2	C90978	IS629 transposase
263	54.5	11.8	373	2	G85355	nodulin-like prote	336	53.5	11.6	296	2	H85824	IS629 transposase
264	54.5	11.8	393	2	AB0035	cyathionine beta	337	53.5	11.6	303	2	T13598	trypsin homolog -
265	54.5	11.8	422	2	T07967	mandelonitrile lya	338	53.5	11.6	307	2	B87292	conserved hypothet
266	54.5	11.8	445	1	S54140	D-serine permease	339	53.5	11.6	339	2	H71265	hypothetical prote
267	54.5	11.8	458	1	Y7BSRT	tetracycline resis	340	53.5	11.6	346	2	D70558	probable cyd8 prot
268	54.5	11.8	458	1	Y7SOG	tetracycline resis	341	53.5	11.6	357	2	F81679	cholesterol synthas
269	54.5	11.8	458	1	Y7BSU6	tetracycline resis	342	53.5	11.6	376	2	AF1943	multidrug-efflux t
270	54.5	11.8	458	2	J01211	tetracycline resis	343	53.5	11.6	378	2	T34372	hypothetical prote
271	54.5	11.8	458	2	S23743	tetracycline resis	344	53.5	11.6	383	2	T48018	hypothetical prote
272	54.5	11.8	483	1	A53595	allantoicase (EC 3	345	53.5	11.6	410	2	A48585	transcription fact
273	54.5	11.8	484	2	T00158	amidase (EC 3.5.-	346	53.5	11.6	412	2	AH3274	phycocyanin-like p
274	54.5	11.8	501	2	E87239	aldehyde dehydroge	347	53.5	11.6	461	2	T06936	phycocyanin-like p
275	54.5	11.8	576	2	A49933	protease SM tron	348	53.5	11.6	495	2	I57680	potassium channel
276	54.5	11.8	586	2	T48672	ABC-type transport	349	53.5	11.6	495	2	A40090	potassium channel
277	54.5	11.8	622	2	AC1236	acyltansferase (c	350	53.5	11.6	495	2	B39113	potassium channel
278	54.5	11.8	628	2	T01467	hypothetical prote	351	53.5	11.6	529	2	H84049	hypothetical prote
279	54.5	11.8	722	2	B71728	probable peptidase	352	53.5	11.6	539	2	T33693	hypothetical prote
280	54.5	11.8	735	2	E69139	hypothetical prote	353	53.5	11.6	546	2	S47300	gene F protein - r
281	54.5	11.8	895	2	I54343	dyerophan-assoca	354	53.5	11.6	553	1	VGNZWV	cell fusion glycop
282	54.5	11.8	895	2	S20582	pyruvate phosphate	355	53.5	11.6	556	2	T03114	segment protein -
283	54.5	11.8	900	2	G87431	heterocyst differe	356	53.5	11.6	571	1	H65169	probable transport
284	54.5	11.8	1044	2	AB2158	heterocyst differe	357	53.5	11.6	571	2	D91206	probable cotranspo
285	54.5	11.8	1044	2	AB2158	S-layer protein pr	358	53.5	11.6	594	2	T43246	amino acid transp
286	54.5	11.8	1099	2	T14850	protein-tyrosine k	359	53.5	11.6	594	2	AH2351	serine/threonine k
287	54.5	11.8	1146	2	B35962	protein-tyrosine k	360	53.5	11.6	597	2	T35237	probable secreted
288	54.5	11.8	1182	2	A35962	NADH2 dehydrogenas	361	53.5	11.6	890	2	S30398	aminopeptidase N h
289	54	11.7	98	2	T11783	NADH2 dehydrogenas	362	53.5	11.6	945	2	T10339	DNA-directed DNA p
290	54	11.7	98	2	T11783	NADH2 dehydrogenas	363	53.5	11.6	985	2	T10339	hypothetical prote
291	54	11.7	154	1	MMBE16	16.9K membrane pro	364	53.5	11.6	1045	2	E90705	hypothetical prote
292	54	11.7	168	2	S47881	NADH2 dehydrogenas	365	53.5	11.6	1045	2	H85555	hypothetical prote
293	54	11.7	188	2	A75382	hypothetical prote	366	53.5	11.6	1047	2	E64790	YbdE protein - Bac
294	54	11.7	248	1	PRMSC2	granzyme C (EC 3.4	367	53.5	11.6	1075	2	S76432	cation efflux syst
295	54	11.7	259	2	C64481	conserved hypothet	368	53.5	11.6	1175	2	S51005	protein-tyrosine-p
296	54	11.7	292	2	T14627	hypothetical prote	369	53.5	11.6	2037	2	T16881	hypothetical prote
297	54	11.7	316	2	F91044	transaldolase A (I	370	53.5	11.6	3566	1	A40701	tenascin-X precurs
298	54	11.7	316	2	A85889	transaldolase A (I	371	53	11.5	148	2	T33692	similar to avrRpt2
299	54	11.7	316	2	G65021	transaldolase (EC	372	53	11.5	154	1	F70002	conserved hypothet
300	54	11.7	328	2	A69218	hypothetical prote	373	53	11.5	166	2	D58889	NADH2 dehydrogenas
301	54	11.7	346	2	C86413	cysteine proteinas	374	53	11.5	201	2	A71124	hypothetical prote
302	54	11.7	351	2	I68620	rod outer segment	375	53	11.5	202	2	JC6205	cell surface antiq
303	54	11.7	356	2	S66348	cysteine proteinas	376	53	11.5	210	2	JC5448	serine protease
304	54	11.7	356	2	B97742	hypothetical prote	377	53	11.5	214	2	AH0265	probable membrane
305	54	11.7	386	2	F69061	hypothetical prote	378	53	11.5	216	2	UC7930	small neutral amin
306	54	11.7	386	2	A72313	hypothetical prote	379	53	11.5	224	2	S67949	beta-tubulin ASL1
307	54	11.7	394	2	C64185	cell division prot	380	53	11.5	224	2	S67949	beta-tubulin ASL1
308	54	11.7	428	2	S08084	gene IV protein -	381	53	11.5	224	2	S73823	MG243 homolog H91
309	54	11.7	440	2	E84118	UDP-N-acetylglucos	382	53	11.5	264	2	D71544	hypothetical prote
310	54	11.7	456	2	TA00551	proline-specific p	383	53	11.5	264	2	A75076	membrane protein p
311	54	11.7	476	2	T40086	hypothetical prote	384	53	11.5	279	2	A95933	probable inositol
312	54	11.7	549	2	C86692	peptide-binding pr	385	53	11.5	300	2	B83100	inhibitor of chrom
313	54	11.7	578	2	AE1236	glycerol 3 phospho	386	53	11.5	306	2	D88040	protein P47F6.1 (I
314	54	11.7	573	1	S33212	IND1 protein - fu	387	53	11.5	310	2	D87704	integral membrane
315	54	11.7	604	2	B84221	hypothetical prote	388	53	11.5	332	2	AC0165	L-allo-threonine a
316	54	11.7	625	2	T25373	hypothetical prote	389	53	11.5	349	2	A44965	cysteine proteinas
317	54	11.7	634	2	T33528	hypothetical prote	390	53	11.5	364	2	A45524	antiradicate phosph
318	54	11.7	787	2	T38224	probable glycosyl	391	53	11.5	364	2	AH1857	antiradicate phosph
319	54	11.7	869	2	A96558	probable protein k	392	53	11.5	376	2	E95879	probable sugar ABC
320	54	11.7	880	2	S49627	regulatory protein	393	53	11.5	377	2	A53044	geranylgeranyl-dip
321	54	11.7	885	2	G83260	aminopeptidase N p	394	53	11.5	385	2	A91178	probable membrane

395	53	11.5	385	2	B86024	probable membrane	468	52.5	11.4	409	2	T47644	protein phosphatas
396	53	11.5	385	2	S47733	ytlu protein precu	469	52.5	11.4	410	2	B48585	transcription fact
397	53	11.5	386	2	A26017	patatin T5 precurs	470	52.5	11.4	421	2	T35515	hypothetical prote
398	53	11.5	403	2	E69873	cell-division prot	471	52.5	11.4	422	2	JE0239	lin-10 protein - r
399	53	11.5	405	2	S61551	breast-regressing	472	52.5	11.4	422	2	B82904	hypothetical prote
400	53	11.5	409	2	P83483	probable MPS trans	473	52.5	11.4	429	2	AP0681	probable voltage g
401	53	11.5	418	2	B82087	MPC family protei	474	52.5	11.4	429	2	S30049	transcription fact
402	53	11.5	426	2	B82712	ATP-dependent Clp	475	52.5	11.4	452	2	G95356	probable oxidoredu
403	53	11.5	438	2	G87675	arylesterase-relat	476	52.5	11.4	500	2	H70629	probable AMINOPEPT
404	53	11.5	447	2	H65343	hypothetical prote	477	52.5	11.4	514	2	T21286	hypothetical prote
405	53	11.5	447	2	H72089	hypothetical prote	478	52.5	11.4	523	2	SS1401	probable membrane
406	53	11.5	463	2	B81580	hypothetical prote	479	52.5	11.4	533	1	YRMSCS	monophenol monooxy
407	53	11.5	469	1	AJEBQT	glutamate-ammonia	480	52.5	11.4	532	2	AH2191	hypothetical prote
408	53	11.5	469	2	A10949	glutamate-ammonia	481	52.5	11.4	542	2	A13564	hypothetical membr
409	53	11.5	469	2	S23899	glutamate-ammonia	482	52.5	11.4	546	2	B32688	beta-galactosidase
410	53	11.5	471	2	S78347	photoeystem II chl	483	52.5	11.4	549	2	G91178	cytoplasmic trehal
411	53	11.5	515	2	B84406	TPK potassium upa	484	52.5	11.4	549	2	H86024	cytoplasmic trehal
412	53	11.5	581	2	T38501	hypothetical prote	485	52.5	11.4	549	2	S47739	probable alpha,alp
413	53	11.5	586	2	T20036	hypothetical prote	486	52.5	11.4	572	2	A56676	excitatory amino a
414	53	11.5	588	2	AC2276	oligopeptide bindi	487	52.5	11.4	652	2	AH2245	2',3'-cyclic-nucle
415	53	11.5	605	2	E69153	cadmium efflux ATP	488	52.5	11.4	657	1	A64079	hypothetical prote
416	53	11.5	610	2	A55939	dhhydroliipoamide S	489	52.5	11.4	666	2	T06700	NADH2 dehydrogenas
417	53	11.5	618	2	A13303	dhhydroliipoamide S	490	52.5	11.4	699	2	T12170	NADH2 dehydrogenas
418	53	11.5	637	2	T49099	dhhydroliipoamide S	491	52.5	11.4	699	2	T12172	NADH2 dehydrogenas
419	53	11.5	653	2	A83154	probable choline t	492	52.5	11.4	699	2	T12173	NADH2 dehydrogenas
420	53	11.5	656	2	T52064	dnaf-like protein	493	52.5	11.4	795	1	SYECFB	NADH2 dehydrogenas
421	53	11.5	728	2	D86278	hypothetical prote	494	52.5	11.4	795	1	H85779	phenylalanine-cRNA
422	53	11.5	770	2	T23999	hypothetical prote	495	52.5	11.4	795	2	D90931	phenylalanine-cRNA
423	53	11.5	776	2	T02584	probable protein k	496	52.5	11.4	803	2	F83360	glucose dehydrogen
424	53	11.5	1005	2	B82969	barcosine oxidase	497	52.5	11.4	826	2	E90289	malate synthase, p
425	53	11.5	1070	2	UC4593	protein-tyrosine k	498	52.5	11.4	883	2	AE0207	conserved hypotnet
426	53	11.5	1162	2	E84431	probable Na+/H+ an	499	52.5	11.4	977	2	T41289	hypothetical prote
427	53	11.5	1176	2	E58345	protein tyrosine p	500	52.5	11.4	1011	2	T40851	hypothetical prote
428	53	11.5	1240	1	DJBE21	DNA-directed DNA p	501	52.5	11.4	1205	2	T18517	hypocellular N-endo
429	53	11.5	1250	2	T00454	hypothetical prote	502	52.5	11.4	1225	2	S24284	E2 glycoprotein pr
430	53	11.5	1305	2	T23314	hypothetical prote	503	52.5	11.4	1225	2	A36607	major capsid prote
431	53	11.5	1326	2	B56395	secretory phosphol	504	52.5	11.4	1345	1	VCBEH6	spike protein - ca
432	53	11.5	1331	2	A56501	calcium channel al	505	52.5	11.4	1453	2	S41453	pipecolate-incorpo
433	53	11.5	1465	2	A56395	secretory phosphol	506	52.5	11.4	1541	2	T30227	hypocellular prote
434	53	11.5	1529	2	T16779	hypothetical prote	507	52.5	11.4	1544	2	T29482	DNA-directed DNA p
435	53	11.5	2143	2	JH0427	voltage-dependent	508	52.5	11.4	2285	1	G02434	hypocellular prote
436	53	11.5	2166	2	S11339	calcium channel pr	509	52	11.3	119	2	D64611	hypocellular prote
437	53	11.5	2171	2	S05054	calcium channel al	510	52	11.3	122	2	F75351	hypocellular prote
438	53	11.5	2199	2	A56616	unknown protein F1	511	52	11.3	148	2	D64356	conserved hypotnet
439	53	11.5	2599	2	I50439	vitelllogenin III -	512	52	11.3	160	2	G95113	regulatory protein
440	52.5	11.4	78	2	G64333	hypothetical prote	513	52	11.3	160	2	H97982	hypocellular prote
441	52.5	11.4	159	2	B85360	ribosomal protein	514	52	11.3	175	2	AE1508	hypocellular prote
442	52.5	11.4	165	2	C72116	hypothetical prote	515	52	11.3	202	2	UC4635	tumor-associated L
443	52.5	11.4	210	2	A83516	probable outer mem	516	52	11.3	207	2	T45600	hypocellular prote
444	52.5	11.4	219	2	F75402	probable competenc	517	52	11.3	219	2	G97271	probable phosphogl
445	52.5	11.4	219	2	AC1881	hypothetical prote	518	52	11.3	235	2	E82173	pseudouridine synt
446	52.5	11.4	244	2	S29982	class II histocomp	519	52	11.3	238	2	C82866	conjugal transfer
447	52.5	11.4	245	2	S29980	class II histocomp	520	52	11.3	260	2	I56559	neuropain - mouse
448	52.5	11.4	256	2	S14518	chlorophyll a/b-bl	521	52	11.3	262	2	B81200	conserved hypotnet
449	52.5	11.4	257	2	S29981	class II histocomp	522	52	11.3	265	2	D83761	hypocellular prote
450	52.5	11.4	285	1	A43556	homeotic protein H	523	52	11.3	291	2	B75618	chromosome partiti
451	52.5	11.4	289	2	E64330	dhhydrodiplicolnat	524	52	11.3	295	2	E85661	probable transposa
452	52.5	11.4	296	2	S09261	probable transposas	525	52	11.3	297	2	T47857	myb protein-like -
453	52.5	11.4	301	2	B64189	glycine cleavage s	526	52	11.3	310	2	S46239	ribosome-inactivat
454	52.5	11.4	309	2	A87564	membrane protein,	527	52	11.3	310	2	T32006	hypocellular prote
455	52.5	11.4	310	2	C39778	legatose-6-phospha	528	52	11.3	320	2	A12305	hypocellular prote
456	52.5	11.4	310	2	T31125	hypocellular prote	529	52	11.3	327	2	AH2608	transcription regu
457	52.5	11.4	322	2	AF1031	hypocellular prote	530	52	11.3	327	2	G97390	arac family transc
458	52.5	11.4	332	2	C72310	conserved hypotnet	531	52	11.3	359	2	A43532	B-cell surface ant
459	52.5	11.4	334	2	D81217	hypocellular prote	532	52	11.3	364	2	B71139	hypocellular prote
460	52.5	11.4	334	2	T13950	hypocellular prote	533	52	11.3	372	2	B64819	probable membrane
461	52.5	11.4	342	2	C48435	cysteine proteinas	534	52	11.3	372	2	B85591	hypocellular prote
462	52.5	11.4	356	2	D84280	hypocellular prote	535	52	11.3	372	2	G90740	hypocellular prote
463	52.5	11.4	366	2	T51344	RNA helicase RH18	536	52	11.3	375	2	S47704	hypocellular 41.1K
464	52.5	11.4	366	2	A49877	prostaglandin F re	537	52	11.3	375	2	F91173	probable transpor
465	52.5	11.4	377	2	G69758	amino acid transpo	538	52	11.3	379	2	F86019	hypocellular prote
466	52.5	11.4	394	2	B86507	hypocellular prote	539	52	11.3	397	2	F83152	conserved hypotnet
467	52.5	11.4	394	2	B81554	hypocellular prote	540	52	11.3	397	2	B70048	conserved hypotnet

541	52	11.3	417	2	B69804	614	51.5	11.2	410	2	S45894	regulatory protein
542	52	11.3	457	2	S39079	615	51.5	11.2	429	2	F87038	probable membrane
543	52	11.3	469	2	D81017	616	51.5	11.2	438	2	A83037	probable MFS trans
544	52	11.3	470	2	C70641	617	51.5	11.2	450	2	C96704	unknown protein, 2
545	52	11.3	491	2	S75449	618	51.5	11.2	451	2	F75177	tryptophan synthas
546	52	11.3	502	2	G87433	619	51.5	11.2	474	1	A40570	lipoprotein lipase
547	52	11.3	502	2	T29729	620	51.5	11.2	478	1	C42790	cystathionine beta
548	52	11.3	526	2	H85891	621	51.5	11.2	478	1	C30763	hypothetical prote
549	52	11.3	526	2	D91047	622	51.5	11.2	478	2	T32476	probable protein-t
550	52	11.3	530	2	D87255	623	51.5	11.2	481	2	B82130	pyruvate kinase II
551	52	11.3	534	2	T27054	624	51.5	11.2	493	2	T21445	hypothetical prote
552	52	11.3	544	2	T17422	625	51.5	11.2	503	2	G82409	glyceroldehyde 3-p
553	52	11.3	548	2	C82698	626	51.5	11.2	519	2	T34546	hypothetical prote
554	52	11.3	553	2	S75892	627	51.5	11.2	525	2	A70735	probable guaA prot
555	52	11.3	567	2	H87370	628	51.5	11.2	531	2	D96965	PTS system, arbuti
556	52	11.3	573	2	A33533	629	51.5	11.2	534	1	TJ00274	cell fusion glycop
557	52	11.3	579	2	H64100	630	51.5	11.2	536	2	D81700	CTP synthase TC05
558	52	11.3	635	2	H65626	631	51.5	11.2	536	2	F85697	hypothetical prote
559	52	11.3	706	2	H81943	632	51.5	11.2	536	2	D64865	probable Na+/H+-ex
560	52	11.3	707	2	C81161	633	51.5	11.2	536	2	F90839	hypothetical prote
561	52	11.3	733	2	F83965	634	51.5	11.2	540	1	TJ00470	site-specific DNA-
562	52	11.3	738	2	S37876	635	51.5	11.2	541	1	A70022	multidrug-efflux t
563	52	11.3	773	2	AH2061	636	51.5	11.2	541	2	UN0511	heat shock protein
564	52	11.3	823	2	A96737	637	51.5	11.2	547	2	T46059	MAP kinase - Arabi
565	52	11.3	840	2	T21333	638	51.5	11.2	549	2	T51099	MAP kinase import
566	52	11.3	869	2	A95156	639	51.5	11.2	550	1	E48556	cell fusion glycop
567	52	11.3	878	2	D98022	640	51.5	11.2	558	2	C72391	conserved hypothet
568	52	11.3	906	2	A82533	641	51.5	11.2	560	2	S27387	interferon alpha r
569	52	11.3	1016	2	T00375	642	51.5	11.2	561	1	A42790	cycatthionine beta
570	52	11.3	1017	2	T37201	643	51.5	11.2	623	2	T35377	probable membrane
571	52	11.3	1106	2	A97647	644	51.5	11.2	666	2	AF0815	transketolase (EC
572	52	11.3	1106	2	AC2870	645	51.5	11.2	667	1	A48660	transketolase (EC
573	52	11.3	1146	2	T09312	646	51.5	11.2	667	2	G91044	transketolase 2 is
574	52	11.3	1146	2	A82174	647	51.5	11.2	667	2	B85889	transketolase 2 is
575	52	11.3	1484	2	C97196	648	51.5	11.2	682	2	T12715	NAHD2 dehydrogenas
576	52	11.3	1957	2	S68453	649	51.5	11.2	724	2	T19601	hypothetical prote
577	52	11.3	2139	2	A44467	650	51.5	11.2	726	2	T31287	hypothetical prote
578	52	11.3	2220	2	A45290	651	51.5	11.2	763	2	A13443	Na+/H+ antiporter
579	52	11.3	2429	2	T13853	652	51.5	11.2	765	2	B75288	hypothetical prote
580	51.5	11.2	116	2	A83693	653	51.5	11.2	795	2	A80705	phenylalanyl-tRNA
581	51.5	11.2	122	1	PSABA	654	51.5	11.2	829	2	T29372	hypothetical prote
582	51.5	11.2	131	1	C72563	655	51.5	11.2	846	2	T27282	hypothetical prote
583	51.5	11.2	146	2	S42570	656	51.5	11.2	869	2	C56617	cifac protein precu
584	51.5	11.2	167	2	H86784	657	51.5	11.2	1451	1	J01719	E2 glycoprotein pr
585	51.5	11.2	172	2	F75491	658	51.5	11.2	1755	2	T51532	hypothetical prote
586	51.5	11.2	206	1	I40173	659	51.5	11.2	1784	2	T43167	sodium channel pro
587	51.5	11.2	209	2	T00733	660	51.5	11.2	2301	1	GNNYTN	genome polypeptin
588	51.5	11.2	212	1	A49436	661	51.5	11.2	2303	1	GNNYTM	genome polypeptin
589	51.5	11.2	222	2	H64495	662	51.5	11.1	89	2	AH3403	hypothetical prote
590	51.5	11.2	270	2	A29934	663	51.5	11.1	93	2	A86491	CT001 hypothetical
591	51.5	11.2	276	2	A70425	664	51.5	11.1	93	2	F72130	conserved hypothet
592	51.5	11.2	282	2	AC2294	665	51.5	11.1	95	2	A62439	hypothetical prote
593	51.5	11.2	289	2	G97192	666	51.5	11.1	97	2	C75415	hypothetical prote
594	51.5	11.2	299	2	B95939	667	51.5	11.1	106	2	A72588	hypothetical prote
595	51.5	11.2	329	2	H97884	668	51.5	11.1	152	2	H95153	conserved hypothet
596	51.5	11.2	322	2	B69170	669	51.5	11.1	173	2	AF2518	hypothetical prote
597	51.5	11.2	313	2	S75329	670	51.5	11.1	188	2	T15651	hypothetical prote
598	51.5	11.2	314	2	T21971	671	51.5	11.1	201	2	B75039	multiple antibiotic
599	51.5	11.2	319	2	T02691	672	51.5	11.1	202	2	A81441	probable orotate p
600	51.5	11.2	342	2	T16806	673	51.5	11.1	204	2	A82389	conserved hypothet
601	51.5	11.2	355	2	S76667	674	51.5	11.1	212	2	I67437	cysteine proteins
602	51.5	11.2	364	2	G83734	675	51.5	11.1	221	2	S75146	hypothetical prote
603	51.5	11.2	366	2	I53488	676	51.5	11.1	229	2	B85806	hypothetical prote
604	51.5	11.2	366	2	S51281	677	51.5	11.1	229	2	D90958	hypothetical prote
605	51.5	11.2	370	2	AH1485	678	51.5	11.1	240	2	T02059	GRP-binding regula
606	51.5	11.2	370	2	AH1124	679	51.5	11.1	246	2	S26826	histone H1 - maize
607	51.5	11.2	376	2	A75381	680	51.5	11.1	246	2	T28166	hypothetical prote
608	51.5	11.2	380	2	D83174	681	51.5	11.1	261	2	A71192	probable glucose 1
609	51.5	11.2	381	2	A35300	682	51.5	11.1	263	2	AC9280	glutathione S-tran
610	51.5	11.2	381	2	F87553	683	51.5	11.1	264	2	G86978	uncharacterized co
611	51.5	11.2	382	2	H84971	684	51.5	11.1	265	2	B81229	phosphatidate cycl
612	51.5	11.2	383	2	I53870	685	51.5	11.1	265	2	A82000	phosphatidate cycl
613	51.5	11.2	390	2	C95954	686	51.5	11.1	268	2	S03328	embryonic abundant

687	51	11.1	279	2	T22051	hypothetical prote	760	50.5	11.0	173	2	S59864	TRAP-like protein
688	51	11.1	282	2	E64063	hypothetical prote	761	50.5	11.0	201	1	IMBPSB	immunity protein -
689	51	11.1	282	2	A41025	aspergillopepsin I	762	50.5	11.0	204	2	E83036	hypothetical prote
690	51	11.1	285	2	T15498	hypothetical prote	763	50.5	11.0	208	2	F71314	probable transcrip
691	51	11.1	295	2	F90938	hypothetical prote	764	50.5	11.0	217	2	I51062	MHC class II beta
692	51	11.1	295	2	B85664	transposase for IS	765	50.5	11.0	224	2	T34686	probable integral
693	51	11.1	295	2	D90801	hypothetical prote	766	50.5	11.0	227	2	T12797	immunity protein d
694	51	11.1	295	2	B85613	probable transpos	767	50.5	11.0	228	2	C28551	hypothetical prote
695	51	11.1	309	2	AF0746	mobility protein B	768	50.5	11.0	231	2	H81698	hypothetical prote
696	51	11.1	321	2	A55090	cahepsin O (EC 3.	769	50.5	11.0	233	2	JH0372	42K surface glycop
697	51	11.1	328	1	S64306	hypothetical prote	770	50.5	11.0	234	2	E95360	hypothetical prote
698	51	11.1	348	1	AG0645	spermidine/putresc	771	50.5	11.0	240	1	TQEC34	transposase - Bsch
699	51	11.1	355	2	B96785	protein F10A5.28 (772	50.5	11.0	247	1	I51060	MHC class II beta
700	51	11.1	357	2	A71523	probable chorismat	773	50.5	11.0	247	2	I51059	MHC class II beta
701	51	11.1	361	2	A45211	prostaglandin E re	774	50.5	11.0	249	2	S75671	hypothetical prote
702	51	11.1	362	2	A53058	prostaglandin F2-a	775	50.5	11.0	249	2	H95256	ABC transporter, p
703	51	11.1	364	2	S65009	prostaglandin E re	776	50.5	11.0	250	2	T09160	proteasome subunit
704	51	11.1	365	2	A42414	prostaglandin E re	777	50.5	11.0	252	2	F70711	probable membran
705	51	11.1	372	2	S75587	H+/Ca2+ exchanging	778	50.5	11.0	253	2	A98132	hypothetical prote
706	51	11.1	375	2	T03256	GTP-binding protei	779	50.5	11.0	255	2	JN0829	3alpha-hydroxyster
707	51	11.1	377	2	T04086	GTP-binding protei	780	50.5	11.0	258	2	A69805	hypothetical prote
708	51	11.1	377	2	T16985	conserved hypotet	781	50.5	11.0	260	2	F82954	probable short-cha
709	51	11.1	379	2	AB2423	hypothetical prote	782	50.5	11.0	264	2	D87504	hypothetical prote
710	51	11.1	384	2	A69622	ferrichrome ABC tr	783	50.5	11.0	266	2	E86844	shikimate 5-dehydr
711	51	11.1	394	2	B85535	probable transport	784	50.5	11.0	288	2	F85818	hypothetical prote
712	51	11.1	394	2	F90684	probable transport	785	50.5	11.0	293	2	A83623	hypothetical prote
713	51	11.1	402	2	B82491	MupC family protei	786	50.5	11.0	296	2	A85841	probable transpos
714	51	11.1	404	2	T39270	conserved hypotet	787	50.5	11.0	296	2	D91284	hypothetical prote
715	51	11.1	409	2	G90491	conserved hypotet	788	50.5	11.0	296	2	F90868	hypothetical prote
716	51	11.1	416	2	T14554	calreticulin - bee	789	50.5	11.0	296	2	D90955	hypothetical prote
717	51	11.1	418	2	S31124	hypothetical prote	790	50.5	11.0	296	2	E91020	hypothetical prote
718	51	11.1	421	2	B82062	conserved hypotet	791	50.5	11.0	296	2	A91132	hypothetical prote
719	51	11.1	423	2	AB0054	probable Na+ depen	792	50.5	11.0	296	2	F91111	hypothetical prote
720	51	11.1	435	2	E71350	probable aspartate	793	50.5	11.0	296	2	G90998	hypothetical prote
721	51	11.1	439	2	S58327	cobalt accumulat	794	50.5	11.0	296	2	T00240	transposase - Bsch
722	51	11.1	439	2	T18898	hypothetical prote	795	50.5	11.0	296	2	B90837	hypothetical prote
723	51	11.1	440	2	AD1073	thymidine phosphor	796	50.5	11.0	296	2	C91065	hypothetical prote
724	51	11.1	449	2	C86496	hypothetical prote	797	50.5	11.0	296	2	H90779	hypothetical prote
725	51	11.1	449	2	D72127	hypothetical prote	798	50.5	11.0	296	2	C90906	hypothetical prote
726	51	11.1	449	2	A81544	hypothetical prote	799	50.5	11.0	296	2	A99972	hypothetical prote
727	51	11.1	450	2	AB1420	PTS cellobiose-spe	800	50.5	11.0	297	2	T09542	endonuclease G (EC
728	51	11.1	450	2	AC11795	PTS cellobiose-spe	801	50.5	11.0	297	2	T45436	hypothetical membr
729	51	11.1	458	1	YTB318	tetracycline resis	802	50.5	11.0	302	2	S02728	actindatin (EC 3.4
730	51	11.1	460	2	S06469	photoeystem II chl	803	50.5	11.0	302	2	S60955	probable membrane
731	51	11.1	466	2	B84132	aminopeptidase B3	804	50.5	11.0	313	2	AH1300	malonyl CoA-acyl c
732	51	11.1	468	2	A69468	ammonium transport	805	50.5	11.0	314	2	F86928	34 kDa antigen (im
733	51	11.1	485	2	A72006	arginine/ornithine	806	50.5	11.0	317	2	T27994	hypothetical prote
734	51	11.1	514	2	A86671	Ammonium transport	807	50.5	11.0	324	2	A86839	conserved hypotet
735	51	11.1	516	2	T09859	cytochrome-c oxida	808	50.5	11.0	327	2	S61982	probable membrane
736	51	11.1	525	2	T00459	hypothetical prote	809	50.5	11.0	332	2	S77386	nitratre transport
737	51	11.1	528	2	T22583	hypothetical prote	810	50.5	11.0	346	2	C71390	NMDH2 dehydrogen
738	51	11.1	531	2	T12406	cytochrome-c oxida	811	50.5	11.0	351	2	A69808	H+/Ca2+ exchanger
739	51	11.1	560	2	T51485	sugar transporter-	812	50.5	11.0	355	1	BVECMG	UDP-N-acetylgluc
740	51	11.1	616	2	T07611	aconitate hydrat	813	50.5	11.0	355	2	F85491	hypothetical prote
741	51	11.1	635	1	A64162	cytochrome c-type	814	50.5	11.0	355	2	F90640	hypothetical prote
742	51	11.1	639	2	J00607	glucan 1,4-alpha-g	815	50.5	11.0	361	2	F87286	cation efflux fami
743	51	11.1	699	2	A96802	unknown protein [i	816	50.5	11.0	362	2	JC7559	ephingosine 1-phos
744	51	11.1	745	1	A70458	phosphoribosylform	817	50.5	11.0	364	2	H70776	hypothetical prote
745	51	11.1	754	1	A39329	phospholipase A2 (818	50.5	11.0	377	2	B51064	geranylgeranyl-dip
746	51	11.1	754	2	S37403	transcription fact	819	50.5	11.0	379	2	T45768	protein phosphat
747	51	11.1	770	2	T50308	probable translati	820	50.5	11.0	382	2	H90500	glycolate oxidase
748	51	11.1	778	2	E97224	ATP-dependent Lon	821	50.5	11.0	398	2	S75202	hypothetical prote
749	51	11.1	854	2	T23837	hypothetical prote	822	50.5	11.0	399	2	T26257	hypothetical prote
750	51	11.1	862	2	T46289	hypothetical prote	823	50.5	11.0	406	2	T27947	hypothetical prote
751	51	11.1	873	2	T16282	hypothetical prote	824	50.5	11.0	407	2	E70309	hypothetical prote
752	51	11.1	887	2	T01113	translaction initia	825	50.5	11.0	408	2	T29949	hypothetical prote
753	51	11.1	967	2	A30325	membrane alanyl am	826	50.5	11.0	410	2	UC7584	basic helix-loop-h
754	51	11.1	1075	2	D70568	hypothetical prote	827	50.5	11.0	411	2	AG3003	conserved hypotet
755	51	11.1	1325	2	A64905	yakC protein - Bsc	828	50.5	11.0	421	2	B98280	hypothetical prote
756	51	11.1	1790	1	S27772	vitellogenin precu	829	50.5	11.0	421	2	D70868	probable lipD prot
757	50.5	11.0	137	2	D75337	hypothetical prote	830	50.5	11.0	424	2	A71846	glycinamide ribonu
758	50.5	11.0	141	2	E72580	hypothetical prote	831	50.5	11.0	424	2	B64672	glycinamide ribonu
759	50.5	11.0	155	2	T22027	hypothetical prote	832	50.5	11.0	441	2	AF0411	probable chloride

833	50.5	11.0	442	2	S56057	heavy metal ion re
834	50.5	11.0	448	2	A83775	hypothetical prote
835	50.5	11.0	460	2	G85525	probable deaminase
836	50.5	11.0	460	2	E90675	probable deaminase
837	50.5	11.0	470	2	T20851	hypothetical prote
838	50.5	11.0	471	2	D83546	probable amino aci
839	50.5	11.0	474	1	JH0790	lipoprotein lipase
840	50.5	11.0	507	2	T27627	hypothetical prote
841	50.5	11.0	509	2	G81929	probable iron-prote
842	50.5	11.0	510	2	T20850	hypothetical prote
843	50.5	11.0	515	2	G75267	ABC transporter, p
844	50.5	11.0	517	2	S21042	cytochrome-c oxida
845	50.5	11.0	518	2	S34565	gene G protein - h
846	50.5	11.0	518	2	F70831	probable PPE prote
847	50.5	11.0	520	2	AD2383	Na+/H+-exchanging
848	50.5	11.0	526	2	G83436	hypothetical prote
849	50.5	11.0	529	1	YRHU1	monophenol monooxy
850	50.5	11.0	543	2	T37570	WD repeat protein
851	50.5	11.0	543	2	S65462	glucose transport
852	50.5	11.0	544	2	AD1979	permease protein o
853	50.5	11.0	545	2	AC1914	hypothetical prote
854	50.5	11.0	546	2	B40407	sterol carrier pro
855	50.5	11.0	563	2	S32156	mandelonitrile lya
856	50.5	11.0	577	2	T52608	probable nitrate t
857	50.5	11.0	584	2	S40013	hypothetical prote
858	50.5	11.0	586	2	F84663	probable nitrate t
859	50.5	11.0	595	2	AD2718	aspartyl-L-cRNA synt
860	50.5	11.0	595	2	D97500	aspartyl-L-cRNA synt
861	50.5	11.0	608	2	S76192	hypothetical prote
862	50.5	11.0	684	2	T25603	hypothetical prote
863	50.5	11.0	708	2	H96681	protein F1822.10 (
864	50.5	11.0	708	2	F87706	proyl oligopeptid
865	50.5	11.0	712	2	AD2721	H+ translocating p
866	50.5	11.0	714	2	H97502	h+ translocating p
867	50.5	11.0	731	2	E82922	phosphate transpor
868	50.5	11.0	736	2	AC2821	bacteriophytochrom
869	50.5	11.0	745	2	C97599	cyanobacterial phy
870	50.5	11.0	819	2	F87708	cell division prote
871	50.5	11.0	827	2	A95877	hypothetical prote
872	50.5	11.0	908	2	A10327	two-component regu
873	50.5	11.0	942	1	U01674	protein kinase TWK
874	50.5	11.0	962	2	T05845	hypothetical prote
875	50.5	11.0	1163	1	RMHU1C	cell surface glyco
876	50.5	11.0	1188	2	T20333	hypothetical prote
877	50.5	11.0	1265	2	T47626	structural mainten
878	50.5	11.0	1317	2	T03748	apoptosis associat
879	50.5	11.0	1345	2	T44204	capacid protein U57
880	50.5	11.0	1345	2	T44017	major capacid prote
881	50.5	11.0	1400	2	B70963	hypothetical prote
882	50.5	11.0	1447	1	VGJHE3	E2 glycoprotein pr
883	50.5	11.0	1447	1	VGJHE2	E2 glycoprotein pr
884	50.5	11.0	1449	1	A43573	E2 glycoprotein pr
885	50.5	11.0	1449	1	VGJHFS	E2 glycoprotein pr
886	50.5	11.0	1577	2	T15851	hypothetical prote
887	50.5	11.0	1672	2	C81675	polymorphic membra
888	50.5	11.0	1921	2	T13827	kinasin-73 - fruit
889	50.5	11.0	89	2	H83795	hypothetical prote
890	50.5	11.0	89	2	A12298	cobalt transport p
891	50.5	11.0	102	2	A75417	hypothetical prote
892	50.5	11.0	121	2	B72546	hypothetical prote
893	50.5	11.0	138	2	JC1342	phospholipase A2 (
894	50.5	11.0	147	2	S70109	hypothetical prote
895	50.5	11.0	150	2	G72660	hypothetical prote
896	50.5	11.0	170	2	B86842	hypothetical prote
897	50.5	11.0	175	2	T11179	NADH2 dehydrogenas
898	50.5	11.0	175	2	AE1149	hypothetical prote
899	50.5	11.0	186	2	E82625	outer membrane pro
900	50.5	11.0	195	2	T39603	BAG-family molecul
901	50.5	11.0	203	2	D81934	probable periplasm
902	50.5	11.0	203	2	F81171	cryptic protein NM
903	50.5	11.0	211	2	A47686	bacteriorhodopsin-
904	50.5	11.0	211	2	AC0268	probable exported
905	50.5	11.0	213	2	G75521	ABC transporter, A
906	50.5	10.8	214	2	T10737	extensin-like cell
907	50.5	10.8	216	2	A11441	hypothetical prote
908	50.5	10.8	219	2	T38019	uracil phosphoribo
909	50.5	10.8	232	2	S29001	G protein-coupled
910	50.5	10.8	236	2	T32473	hypothetical prote
911	50.5	10.8	238	2	B64509	hypothetical prote
912	50.5	10.8	250	2	S51206	cruxrhodopsin-1 -
913	50.5	10.8	255	2	A71351	probable cobalt AB
914	50.5	10.8	256	2	A81277	probable oxidoredu
915	50.5	10.8	259	2	C75151	oxidoreductase PAB
916	50.5	10.8	265	2	D81315	hypothetical prote
917	50.5	10.8	265	2	G97460	hypothetical prote
918	50.5	10.8	268	2	C83369	probable binding p
919	50.5	10.8	274	2	E75614	conserved hypochet
920	50.5	10.8	293	2	T36063	probable integral
921	50.5	10.8	295	2	B85787	probable transpos
922	50.5	10.8	295	2	T00315	transposase - Bach
923	50.5	10.8	296	2	167971	transposase - Bach
924	50.5	10.8	296	2	D90398	conserved hypochet
925	50.5	10.8	299	2	S50803	hypothetical prote
926	50.5	10.8	304	2	A72596	hypothetical prote
927	50.5	10.8	308	2	S23928	ubiquinol-cytochro
928	50.5	10.8	314	2	S72525	pectinesterase (EC
929	50.5	10.8	317	2	B87666	homoserine kinase
930	50.5	10.8	332	2	C87426	cysteine synthase
931	50.5	10.8	332	2	C84061	ferrichrome ABC tr
932	50.5	10.8	333	2	T36036	probable integral
933	50.5	10.8	337	2	AC0802	probable semialdeh
934	50.5	10.8	341	2	D48435	cysteine proteinas
935	50.5	10.8	348	2	B86813	dehydrogenase (imp
936	50.5	10.8	357	2	D83685	nicotinate-nucleot
937	50.5	10.8	357	2	T09321	JUN kinase-activat
938	50.5	10.8	372	2	S20056	para-hydroxybenzo
939	50.5	10.8	375	2	T25089	hypothetical prote
940	50.5	10.8	380	2	A71390	ubiquinol-cytochro
941	50.5	10.8	388	2	D69468	ammonium transport
942	50.5	10.8	388	2	AF0183	probable exported
943	50.5	10.8	393	2	S61659	KRPI protein - Yea
944	50.5	10.8	397	2	E91296	probable thymidine
945	50.5	10.8	407	2	F70318	hypothetical prote
946	50.5	10.8	407	2	G75268	hypothetical prote
947	50.5	10.8	414	1	E70708	cytochrome P450 RV
948	50.5	10.8	420	2	A82856	conserved hypochet
949	50.5	10.8	430	2	A12379	hypothetical prote
950	50.5	10.8	435	2	G86907	D-alanyl-D-alanine
951	50.5	10.8	440	1	S56606	thymidine phosphor
952	50.5	10.8	440	2	G86137	Na+-transporting A
953	50.5	10.8	449	2	H69862	chromogranin A pre
954	50.5	10.8	457	1	A28468	streptogrisin C (E
955	50.5	10.8	457	2	A53659	interleukin-6 rece
956	50.5	10.8	460	2	U01145	photosystem II chl
957	50.5	10.8	473	1	F2R244	photosystem II chl
958	50.5	10.8	473	1	F28P44	photosystem II chl
959	50.5	10.8	473	2	T08998	photosystem II pro
960	50.5	10.8	476	2	AC2306	hypothetical prote
961	50.5	10.8	476	2	A11639	multidrug-efflux t
962	50.5	10.8	489	2	C70940	probable cobq prot
963	50.5	10.8	494	2	F98149	hypothetical prote
964	50.5	10.8	514	2	C49507	potassium channel
965	50.5	10.8	516	2	S39686	Na+-dependent sym
966	50.5	10.8	532	2	JC1392	monophenol monooxy
967	50.5	10.8	533	2	AE1138	hypothetical prote
968	50.5	10.8	538	2	C83284	probable biotin-de
969	50.5	10.8	538	2	C86976	ppe-family protein
970	50.5	10.8	539	2	C83758	cephalosporin acyl
971	50.5	10.8	542	2	S50361	probable membrane
972	50.5	10.8	545	2	T18694	hypothetical prote
973	50.5	10.8	545	2	T39499	conserved hypochet
974	50.5	10.8	573	2	D83440	probable sulfate t
975	50.5	10.8	588	2	T25248	hypothetical prote
976	50.5	10.8	598	2	S66669	potassium channel
977	50.5	10.8	602	2	A49507	potassium channel
978	50.5	10.8	602	2	JH0166	potassium voltage-

979	50	10.8	605	2	S57552	hypothetical prote
980	50	10.8	613	2	A56031	potassium channel
981	50	10.8	614	2	E86194	hypothetical prote
982	50	10.8	700	2	B81266	DNA topoisomerase
983	50	10.8	749	1	B39898	phospholipase A2 (
984	50	10.8	756	2	C84682	hypothetical prote
985	50	10.8	789	2	A83688	Na/H+ antiporter
986	50	10.8	789	2	H97469	probable NADH dehy
987	50	10.8	810	1	P2MMBB	2a protein - broad
988	50	10.8	828	1	JC5807	tryp protein - rat
989	50	10.8	828	2	F70363	calcium transportin
990	50	10.8	836	2	C97525	clpA protein (A122
991	50	10.8	836	2	A02744	ATP-dependent Clp
992	50	10.8	876	2	T07101	lipoxigenase (EC 1
993	50	10.8	993	2	F97717	hypothetical prote
994	50	10.8	1015	2	T15830	hypothetical prote
995	50	10.8	1021	2	A86421	Receptor-like seri
996	50	10.8	1022	2	F87635	AcetB/Acro/AcrF fam
997	50	10.8	1277	2	T14152	synaptic scaffoldi
998	50	10.8	1338	2	T40993	protein kinase cek
999	50	10.8	1381	2	T31083	paranodin - rat
1000	50	10.8	1479	2	T42710	mannose receptor,
1001	50	10.8	1498	2	B97355	DNA segregation AT
1002	50	10.8	1505	2	S26765	genome polyprotein
1003	50	10.8	1524	2	S68553	surface layer prot
1004	50	10.8	1526	2	A86528	protein F27015.14
1005	50	10.8	1687	2	S41742	calcium channel al
1006	50	10.8	2109	2	T31352	hypothetical prote
1007	50	10.8	2819	2	A90551	conserved hypother
1008	49.5	10.7	63	2	B90031	hypothetical prote
1009	49.5	10.7	119	2	PH544	Ig H chain v regio
1010	49.5	10.7	130	2	AD2901	hypothetical prote
1011	49.5	10.7	130	2	S67024	probable membrane
1012	49.5	10.7	150	2	F87507	conserved hypother
1013	49.5	10.7	160	2	C35542	ribosomal protein
1014	49.5	10.7	165	2	F97676	succinate dehydrog
1015	49.5	10.7	165	2	S50195	oleosin - rape
1016	49.5	10.7	171	2	S22194	hypothetical prote
1017	49.5	10.7	172	2	T39644	apric protein - Ac
1018	49.5	10.7	197	2	A82056	hypothetical prote
1019	49.5	10.7	214	2	D83881	siderophore (surfa
1020	49.5	10.7	218	2	AC1253	glycine betaine/ca
1021	49.5	10.7	218	2	AT1615	cell division prot
1022	49.5	10.7	226	2	F87449	glycine betaine/ca
1023	49.5	10.7	244	2	E84885	hypothetical prote
1024	49.5	10.7	251	2	AF2281	hypothetical prote
1025	49.5	10.7	252	1	A34702	amphiregulin precu
1026	49.5	10.7	255	2	H81302	probable membrane
1027	49.5	10.7	275	2	H90251	maltose transport
1028	49.5	10.7	294	2	B83040	ribosomal protein
1029	49.5	10.7	295	2	T04483	probable ring fing
1030	49.5	10.7	301	1	S10456	cytochrome c-type
1031	49.5	10.7	302	1	F83392	hypothetical prote
1032	49.5	10.7	305	2	AT0847	iron transport pro
1033	49.5	10.7	313	2	AH1672	malonyl CoA-acyl c
1034	49.5	10.7	315	2	B98226	hypothetical prote
1035	49.5	10.7	315	2	A83060	conserved hypother
1036	49.5	10.7	327	2	T32164	hypothetical prote
1037	49.5	10.7	328	2	AD1916	alcohol dehydrogen
1038	49.5	10.7	330	2	H75353	probable noex prot
1039	49.5	10.7	332	2	T33799	hypothetical prote
1040	49.5	10.7	334	2	T23444	hypothetical prote
1041	49.5	10.7	341	2	C98304	probable oligopept
1042	49.5	10.7	341	2	A82979	hypothetical prote
1043	49.5	10.7	348	2	B48435	cysteine proteinas
1044	49.5	10.7	360	2	B87286	conserved hypother
1045	49.5	10.7	367	2	C68500	group II decarboxy
1046	49.5	10.7	368	1	Q0B8HG	early nuclear anti
1047	49.5	10.7	372	1	D69442	conserved hypother
1048	49.5	10.7	374	1	T39857	spore germination
1049	49.5	10.7	380	1	T21513	hypothetical prote
1050	49.5	10.7	380	1	TAGB	actindinain (BC 3.4
1051	49.5	10.7	391	2	T43987	ppat1, pol processi
1052	49.5	10.7	400	2	T46383	hypothetical prote
1053	49.5	10.7	401	2	D83022	hypothetical prote
1054	49.5	10.7	403	2	T09332	DNA polymerase pro
1055	49.5	10.7	424	2	D75330	probable beta-lact
1056	49.5	10.7	427	2	A49518	kallistatin precu
1057	49.5	10.7	430	1	S32570	mALC protein - Str
1058	49.5	10.7	430	2	AF1356	hypothetical prote
1059	49.5	10.7	430	2	AG1726	hypothetical prote
1060	49.5	10.7	432	2	H64383	Na+ transporter -
1061	49.5	10.7	443	2	AE0309	probable sugar tra
1062	49.5	10.7	469	2	T34645	hypothetical prote
1063	49.5	10.7	469	2	S74825	probable Rieske ir
1064	49.5	10.7	476	1	VMUT4R	variant surface gl
1065	49.5	10.7	476	2	B86829	multidrug transpor
1066	49.5	10.7	478	2	T33942	hypothetical prote
1067	49.5	10.7	502	2	T26256	hypothetical prote
1068	49.5	10.7	505	2	G90419	metabolite permeas
1069	49.5	10.7	508	2	H86474	hypothetical prote
1070	49.5	10.7	514	2	F87592	hypothetical prote
1071	49.5	10.7	524	2	F83429	actin interacting
1072	49.5	10.7	538	2	T40298	membrane transport
1073	49.5	10.7	538	2	A83018	probable sodium/hy
1074	49.5	10.7	552	2	A51027	L-ascorbate oxidas
1075	49.5	10.7	553	2	B90153	2-isopropylmalate
1076	49.5	10.7	556	2	T46882	K+-transporting AT
1077	49.5	10.7	557	2	H97351	K+-transporting AT
1078	49.5	10.7	559	2	C87307	hypothetical prote
1079	49.5	10.7	566	2	B82173	probable ABC trans
1080	49.5	10.7	579	2	S11027	L-ascorbate oxidas
1081	49.5	10.7	583	2	T48473	amino acid transpo
1082	49.5	10.7	583	2	E83794	ABC transporter (A
1083	49.5	10.7	586	1	E69314	replication licens
1084	49.5	10.7	660	2	B97853	NMDH2 dehydrogenas
1085	49.5	10.7	686	2	E71895	probable heavy-met
1086	49.5	10.7	697	2	T13670	NMDH2 dehydrogenas
1087	49.5	10.7	698	2	T13625	NMDH2 dehydrogenas
1088	49.5	10.7	699	2	T12673	NMDH2 dehydrogenas
1089	49.5	10.7	700	2	T23629	hypothetical prote
1090	49.5	10.7	701	2	T13056	NMDH2 dehydrogenas
1091	49.5	10.7	702	2	T13587	NMDH2 dehydrogenas
1092	49.5	10.7	702	2	T13058	NMDH2 dehydrogenas
1093	49.5	10.7	702	2	T12624	NMDH2 dehydrogenas
1094	49.5	10.7	702	2	T13409	NMDH2 dehydrogenas
1095	49.5	10.7	703	2	T13074	NMDH2 dehydrogenas
1096	49.5	10.7	703	2	T13696	NMDH2 dehydrogenas
1097	49.5	10.7	706	2	T12748	NMDH2 dehydrogenas
1098	49.5	10.7	721	2	F82198	probable toxin sec
1099	49.5	10.7	732	2	A83481	probable TonB-depe
1100	49.5	10.7	734	1	DER2N5	NMDH2 dehydrogenas
1101	49.5	10.7	738	2	S58612	NMDH2 dehydrogenas
1102	49.5	10.7	740	2	B84741	hypothetical prote
1103	49.5	10.7	745	2	B84673	hypothetical prote
1104	49.5	10.7	745	2	F69338	pyruvate, water di
1105	49.5	10.7	770	2	S56695	transducin-like en
1106	49.5	10.7	776	2	S45485	leap4 protein - fis
1107	49.5	10.7	788	1	I59282	diacylglycerol kin
1108	49.5	10.7	795	2	D82225	phenylalaninyl-tRNA
1109	49.5	10.7	822	2	T25866	hypothetical prote
1110	49.5	10.7	826	2	AC0086	outer membrane ush
1111	49.5	10.7	850	2	JC5700	EdbB kinase activa
1112	49.5	10.7	875	2	T12794	hypothetical yong
1113	49.5	10.7	888	2	A54280	cell differentiat
1114	49.5	10.7	914	1	JN0550	iodide peroxidase
1115	49.5	10.7	945	2	S77052	cation-transportin
1116	49.5	10.7	1039	2	T38447	tetratricopeptide
1117	49.5	10.7	1069	2	D85383	hypothetical prote
1118	49.5	10.7	1084	2	T15616	hypothetical prote
1119	49.5	10.7	1121	2	UC7329	WD-repeat protein
1120	49.5	10.7	1132	2	T31107	telomerase reverse
1121	49.5	10.7	1163	2	A56097	arylporin-binding
1122	49.5	10.7	1195	2	S76592	5-methyltetrahydro
1123	49.5	10.7	1354	2	AG0538	Rhs-family protein
1124	49.5	10.7	1461	2	E90696	hypothetical prote

1125	49.5	10.7	1461	2	A85547	hypothetical prote	1198	49	10.6	355	2	S41686	geranylgeranyltran
1126	49.5	10.7	1492	2	A39322	cyctic fibrobls tr	1199	49	10.6	366	2	A64950	membrane-bound pen
1127	49.5	10.7	2150	2	T08165	RNA1 polypeptin -	1200	49	10.6	366	2	C58800	probable cytochrom
1128	49.5	10.7	2222	1	A36028	DNA-directed DNA p	1201	49	10.6	366	2	G90951	probable cytochrom
1129	49.5	10.7	2403	2	T30875	PR8 protein homol	1202	49	10.6	367	2	G96770	hypothetical prote
1130	49.5	10.7	2500	1	WMAUE2	HIV-Ep2 enhancer-b	1203	49	10.6	370	2	A80602	probable membrane
1131	49.5	10.7	3655	2	T38084	TRAP-like protein	1204	49	10.6	378	2	F64446	chorismate synthas
1132	49	10.6	98	2	T17363	NADH2 dehydrogenas	1205	49	10.6	379	2	B69332	heterodisulfide re
1133	49	10.6	99	2	T17177	NADH2 dehydrogenas	1206	49	10.6	380	2	T11033	ubiquinol-cytochro
1134	49	10.6	129	2	D75182	1su ribosomal prot	1207	49	10.6	382	2	AH2056	hypothetical prote
1135	49	10.6	135	2	T28983	hypothetical prote	1208	49	10.6	385	2	A86227	hypothetical prote
1136	49	10.6	135	2	F86053	hypothetical prote	1209	49	10.6	391	2	T39673	probable mannosylt
1137	49	10.6	135	2	D91207	hypothetical prote	1210	49	10.6	396	2	T35024	probable glutathio
1138	49	10.6	135	2	A65171	olfs protein - Esc	1211	49	10.6	400	2	C83511	flagellar protein
1139	49	10.6	137	1	JC4877	phospholipase A2 h	1212	49	10.6	404	2	B69662	probable secreted
1140	49	10.6	140	2	S74898	hypothetical prote	1213	49	10.6	408	2	A37813	UDP-N-acetylglucos
1141	49	10.6	146	2	T06471	core protein - gar	1214	49	10.6	411	2	S75327	lysostaphin - Syne
1142	49	10.6	154	2	C71379	probable ATPase, c	1215	49	10.6	419	1	S47692	hypothetical 43.8k
1143	49	10.6	157	2	S18651	variant surface an	1216	49	10.6	419	2	B91169	probable transport
1144	49	10.6	157	2	S58025	probable olfactory	1217	49	10.6	419	2	B86015	hypothetical prote
1145	49	10.6	159	2	S77852	probable phenylala	1218	49	10.6	419	2	G70602	hypothetical prote
1146	49	10.6	160	2	S73261	plastocoulin-plast	1219	49	10.6	425	2	A64977	hypothetical prote
1147	49	10.6	163	2	D71062	hypothetical prote	1220	49	10.6	429	2	B87299	transporter, proba
1148	49	10.6	166	2	D82909	hypothetical prote	1221	49	10.6	431	1	E70699	probable pXa prot
1149	49	10.6	167	2	T11439	NADH2 dehydrogenas	1222	49	10.6	439	2	D72716	hypothetical prote
1150	49	10.6	167	2	B71553	hypothetical prote	1223	49	10.6	441	2	B82023	probable membrane
1151	49	10.6	167	2	A83204	hypothetical prote	1224	49	10.6	444	2	T24076	hypothetical prote
1152	49	10.6	169	2	B75490	hypothetical prote	1225	49	10.6	448	2	A70398	cell division prot
1153	49	10.6	170	2	H71937	3-dehydroquinatate d	1226	49	10.6	450	2	B69934	conserved hypothet
1154	49	10.6	170	2	F90050	hypothetical prote	1227	49	10.6	458	2	AC1173	amino acid transpo
1155	49	10.6	172	2	T33259	hypothetical prote	1228	49	10.6	458	2	AD1530	amino acid transpo
1156	49	10.6	174	2	E90617	NADH dehydrogenase	1229	49	10.6	463	2	C68042	probable transport
1157	49	10.6	179	1	ERAD34	early E3 20.1k gly	1230	49	10.6	463	2	B91195	probable transport
1158	49	10.6	181	2	JX0247	serine proteinase	1231	49	10.6	463	2	H65166	probable transport
1159	49	10.6	185	2	T41299	hypothetical metal	1232	49	10.6	463	2	H69822	sodium-glutamate s
1160	49	10.6	195	2	A82690	conserved hypothet	1233	49	10.6	466	2	G72603	nitrate reductase
1161	49	10.6	195	2	B97472	hypothetical prote	1234	49	10.6	469	1	AJBEQJ	glutamate-ammonta
1162	49	10.6	196	2	T49023	hypothetical prote	1235	49	10.6	469	2	A83356	hypothetical prote
1163	49	10.6	196	2	G87510	hypothetical prote	1236	49	10.6	469	2	G86074	glutamine syntheta
1164	49	10.6	203	2	E72345	endopeptidase Clp	1237	49	10.6	469	2	H91227	glutamine syntheta
1165	49	10.6	203	2	T32745	hypothetical prote	1238	49	10.6	473	2	T07548	photosystem II chl
1166	49	10.6	205	2	T14744	hypothetical prote	1239	49	10.6	475	2	T36342	probable glutamate
1167	49	10.6	207	2	D75341	conserved hypothet	1240	49	10.6	475	2	T06061	cellulase (EC 3.2.
1168	49	10.6	212	2	AC0074	probable tellurium	1241	49	10.6	476	2	H96802	probable amino aci
1169	49	10.6	217	2	B90765	hypothetical prote	1242	49	10.6	485	2	G65051	phosphotransferase
1170	49	10.6	224	2	AG1795	hypothetical prote	1243	49	10.6	485	2	C91075	hypothetical prote
1171	49	10.6	236	2	E81406	hypothetical prote	1244	49	10.6	485	2	B85920	hypothetical prote
1172	49	10.6	244	2	S07398	gamma-gliadin B pr	1245	49	10.6	491	2	B71957	ATP-dependent RNA
1173	49	10.6	255	4	S31866	Ig gamma-1 chain C	1246	49	10.6	492	2	G64550	ATP-dependent RNA
1174	49	10.6	262	2	T48546	hypothetical prote	1247	49	10.6	493	2	A11224	uroporhyrinogen-I
1175	49	10.6	263	2	A82559	transposase all806	1248	49	10.6	493	2	AC1578	uroporhyrinogen-I
1176	49	10.6	276	2	S73410	hypothetical prote	1249	49	10.6	495	1	A26396	T-cell surface gly
1177	49	10.6	287	2	E83928	transcription regu	1250	49	10.6	496	2	F83124	probable transcrip
1178	49	10.6	288	2	AH0247	protein binding-p	1251	49	10.6	507	2	UG0165	LARI protein - hum
1179	49	10.6	300	1	G75436	conserved hypothet	1252	49	10.6	510	2	S51124	probable membrane
1180	49	10.6	308	1	ORECMB	chemotaxis protein	1253	49	10.6	515	2	C58892	cytochrome-c oxida
1181	49	10.6	308	2	C85802	hypothetical prote	1254	49	10.6	516	2	T09949	cytochrome-c oxida
1182	49	10.6	308	2	G90953	chemotaxis protein	1255	49	10.6	522	1	IKEC1	colicin E1 - Esche
1183	49	10.6	308	2	H82936	hpr serine/threoni	1256	49	10.6	526	2	B55024	Hydrogenase-4 comp
1184	49	10.6	312	2	F87335	conserved hypothet	1257	49	10.6	535	2	D96586	hypothetical prote
1185	49	10.6	322	2	A12671	homoserine kinase	1258	49	10.6	542	2	C70732	probable integral
1186	49	10.6	322	2	G97453	homoserine kinase	1259	49	10.6	553	1	H70786	probable dihydrol
1187	49	10.6	324	1	JC4280	carboxyl reductase	1260	49	10.6	555	2	S27163	alpha, alpha-trehal
1188	49	10.6	334	2	T16772	hypothetical prote	1261	49	10.6	557	2	A83040	uracanase (impor
1189	49	10.6	334	2	E87448	arginine-N-succiny	1262	49	10.6	573	2	G98245	hutu gene homolog
1190	49	10.6	335	2	T40292	glyceridehydride 3-p	1263	49	10.6	573	2	S28901	glutamate transpor
1191	49	10.6	337	1	Q0ECH3	probable dehydroge	1264	49	10.6	582	2	S22195	bps2 protein - Des
1192	49	10.6	337	2	C91029	probable PTS syste	1265	49	10.6	586	2	PC6006	scaffolding protei
1193	49	10.6	337	2	D85873	probable PTS syste	1266	49	10.6	597	2	S51212	BAXs protein - bov
1194	49	10.6	345	2	T28026	hypothetical prote	1267	49	10.6	605	2	E70067	conserved hypothet
1195	49	10.6	349	2	C86662	hypothetical prote	1268	49	10.6	605	2	D83007	regulatory protein
1196	49	10.6	352	2	A43113	chemokine (C-C) re	1269	49	10.6	616	2	AG2957	hypothetical prote
1197	49	10.6	353	2	H88939	protein C05E4.13 (1270	49	10.6	616	2	G98325	probable c4-dicar

1271	49	10.6	618	2	F84409
1272	49	10.6	629	2	S29685
1273	49	10.6	642	2	C84944
1274	49	10.6	660	2	T09537
1275	49	10.6	672	2	A65024
1276	49	10.6	672	2	D85891
1277	49	10.6	672	2	D85891
1278	49	10.6	680	2	H91046
1279	49	10.6	719	2	T29871
1280	49	10.6	740	2	S63392
1281	49	10.6	748	1	T03847
1282	49	10.6	784	1	I50699
1283	49	10.6	784	2	U80101
1283	49	10.6	796	2	E87636
1284	49	10.6	799	2	T48690
1285	49	10.6	812	2	AG3138
1286	49	10.6	812	2	D98149
1287	49	10.6	816	2	T21713
1288	49	10.6	839	2	S35319
1289	49	10.6	862	2	S64821
1290	49	10.6	952	2	E84534
1291	49	10.6	969	2	F71418
1292	49	10.6	975	2	T22788
1293	49	10.6	976	2	S40697
1294	49	10.6	1041	2	B81281
1295	49	10.6	1054	2	T30933
1296	49	10.6	1073	1	TYRUMX
1297	49	10.6	1086	2	T40354
1298	49	10.6	1190	2	T00842
1299	49	10.6	1207	2	T52459
1300	49	10.6	1230	2	S47466
1301	49	10.6	1265	2	T51314
1302	49	10.6	1366	2	S36851
1303	49	10.6	1430	2	AF0351
1304	49	10.6	1530	2	E82085
1305	49	10.6	1648	2	F84833
1306	49	10.6	2172	2	T20145
1307	49	10.6	3164	1	MMBHE6
1308	48.5	10.5	73	2	D91146
1309	48.5	10.5	73	2	H85991
1310	48.5	10.5	73	2	E65119
1311	48.5	10.5	75	2	T45361
1312	48.5	10.5	115	1	SRRBG
1313	48.5	10.5	116	2	AD2124
1314	48.5	10.5	139	2	G71033
1315	48.5	10.5	146	1	A47481
1316	48.5	10.5	165	2	A31635
1317	48.5	10.5	171	2	JE0153
1318	48.5	10.5	180	2	T40562
1319	48.5	10.5	183	2	B81237
1320	48.5	10.5	183	2	G82008
1321	48.5	10.5	193	2	C97891
1322	48.5	10.5	198	2	S75989
1323	48.5	10.5	199	2	T38524
1324	48.5	10.5	199	2	A69859
1325	48.5	10.5	208	2	C9697
1326	48.5	10.5	211	2	C59091
1327	48.5	10.5	217	2	A98196
1328	48.5	10.5	221	2	D64907
1329	48.5	10.5	225	2	F81977
1330	48.5	10.5	225	2	A86043
1331	48.5	10.5	226	2	T23233
1332	48.5	10.5	235	2	AC2809
1333	48.5	10.5	235	2	H97587
1334	48.5	10.5	241	2	D84138
1335	48.5	10.5	243	2	B96010
1336	48.5	10.5	243	2	E97425
1337	48.5	10.5	245	2	AE6643
1338	48.5	10.5	256	2	D86544
1339	48.5	10.5	256	2	H72078
1340	48.5	10.5	257	2	A12741
1341	48.5	10.5	257	2	H97522
1342	48.5	10.5	257	2	G87509
1343	48.5	10.5	258	2	H70487

arsenite transport	1344	48.5	10.5	269	2	G87134
retroviral recepto	1345	48.5	10.5	273	2	JS0172
chreomine-trna lig	1346	48.5	10.5	276	2	D41044
xanthophyll epoxid	1347	48.5	10.5	277	2	D64666
hydrogenase-4 comp	1348	48.5	10.5	277	2	G71949
hydrogenase 4 memb	1349	48.5	10.5	278	2	AB2254
hydrogenase 4 memb	1350	48.5	10.5	283	2	B86331
hypothetical prote	1351	48.5	10.5	283	2	D71130
probable membrane	1352	48.5	10.5	290	2	F71167
Fae-binding protei	1353	48.5	10.5	291	2	F81444
cytosolic phosphol	1354	48.5	10.5	302	2	A75432
apolipoprotein B-1	1355	48.5	10.5	312	2	T40201
Tomb-dependent rec	1356	48.5	10.5	318	2	B91177
hypothetical prote	1357	48.5	10.5	330	2	C86023
fimbrial usher pro	1358	48.5	10.5	332	2	AC0260
hypothetical prote	1359	48.5	10.5	334	2	C81794
hypothetical prote	1360	48.5	10.5	340	2	E83126
nucleoporin-intera	1361	48.5	10.5	342	2	E71359
probable membrane	1362	48.5	10.5	355	2	T47527
hypothetical prote	1363	48.5	10.5	365	2	F87552
hypothetical prote	1364	48.5	10.5	370	2	AE0289
hypothetical prote	1365	48.5	10.5	372	2	C39371
processing endopro	1366	48.5	10.5	382	2	A10040
probable secreted	1367	48.5	10.5	387	2	H88012
chitinase (EC 3.2.	1368	48.5	10.5	388	2	T33908
heat-stable entero	1369	48.5	10.5	394	2	AE1940
hypothetical prote	1370	48.5	10.5	398	2	F75417
probable histidine	1371	48.5	10.5	400	2	AG1208
sensory transducti	1372	48.5	10.5	400	2	AB1565
cellulose 1,4-beta	1373	48.5	10.5	401	2	E72339
probable CO-induce	1374	48.5	10.5	406	2	T31778
L-shaped tail fibre	1375	48.5	10.5	409	2	B85735
probable autoclans	1376	48.5	10.5	410	2	C86835
glutamate synthase	1377	48.5	10.5	416	2	T02194
probable SNF2/SW12	1378	48.5	10.5	421	2	E90883
hypothetical prote	1379	48.5	10.5	424	2	T31978
UL6 protein - hum	1380	48.5	10.5	425	2	T25873
hypothetical prote	1381	48.5	10.5	426	2	B75434
hypothetical prote	1382	48.5	10.5	426	2	T45767
hypothetical 7.5 k	1383	48.5	10.5	428	2	J01864
hypothetical prote	1384	48.5	10.5	431	2	H70721
substance P gamma	1385	48.5	10.5	436	2	T39973
hypothetical prote	1386	48.5	10.5	441	2	H89809
hypothetical prote	1387	48.5	10.5	443	2	H70430
interleukin-13 pre	1388	48.5	10.5	461	2	C98120
neural cell adhesi	1389	48.5	10.5	463	2	B81141
mitochondrial inne	1390	48.5	10.5	467	2	T32292
hypothetical 20.1k	1391	48.5	10.5	470	1	F2WU39
hypothetical prote	1392	48.5	10.5	473	2	T17260
probable integral	1393	48.5	10.5	475	2	T08753
hypothetical prote	1394	48.5	10.5	478	2	D64895
hypothetical prote	1395	48.5	10.5	500	2	AD1047
ATP synthase subun	1396	48.5	10.5	509	2	A96563
hypothetical prote	1397	48.5	10.5	510	2	B72007
protein K0289.4 [I	1398	48.5	10.5	511	2	H90439
hypothetical prote	1399	48.5	10.5	518	2	T05196
hypothetical prote	1400	48.5	10.5	528	2	B81186
membrane protein y	1401	48.5	10.5	537	2	A75123
hypothetical prote	1402	48.5	10.5	546	1	VGNZK
probable transposa	1403	48.5	10.5	546	2	S47305
conserved hypotet	1404	48.5	10.5	553	2	C84920
conserved hypotet	1405	48.5	10.5	553	2	T06499
hypothetical 25.1k	1406	48.5	10.5	556	2	S68408
hypothetical prote	1407	48.5	10.5	559	2	C75286
conserved hypotet	1408	48.5	10.5	578	2	B82204
flagellar biosynth	1409	48.5	10.5	583	2	A70723
flagellar biosynth	1410	48.5	10.5	584	1	VCM51A
NAH (ubiquinone)	1411	48.5	10.5	590	2	C86465
conserved sodium-tr	1412	48.5	10.5	598	2	A69609
conserved hypotet	1413	48.5	10.5	601	2	G96558
hypothetical prote	1414	48.5	10.5	605	2	T15291
hypothetical prote	1415	48.5	10.5	608	2	C95255
cytochrome-c oxida	1416	48.5	10.5	610	2	A11110

enoyl-[ACP] reduct	enoyl-1 [ACP] reduct
chlorophyll a/b-bi	chlorophyll a/b-bi
octopone-binding p	octopone-binding p
glutamine ABC tran	glutamine ABC tran
amino acid ABC tra	amino acid ABC tra
hypothetical prote	hypothetical prote
Fe69.15 protein -	Fe69.15 protein -
probable oligopept	probable oligopept
hypothetical prote	hypothetical prote
probable integral	probable integral
3-hydroxybutyryl-C	3-hydroxybutyryl-C
meq protein - Bac	meq protein - Bac
probable hemin per	probable hemin per
hypothetical prote	hypothetical prote
hypothetical phage	hypothetical phage
ferric enterobacti	ferric enterobacti
hypothetical prote	hypothetical prote
hypothetical prote	hypothetical prote
gpII protein (limp	gpII protein (limp
conserved hypotet	conserved hypotet
Ig V-region-like B	Ig V-region-like B
probable methanol	probable methanol
protein K1094.2 [i	protein K1094.2 [i
hypothetical prote	hypothetical prote
two-component resp	two-component resp
L-sorbose dehydr	L-sorbose dehydr
cell-division prot	cell-division prot
hypothetical prote	hypothetical prote
hypothetical prote	hypothetical prote
probable membrane	probable membrane
hypothetical prote	hypothetical prote
hypothetical prote	hypothetical prote
UDP-N-acetylglucos	UDP-N-acetylglucos
hypothetical prote	hypothetical prote
hypothetical 47.0k	hypothetical 47.0k
probable esterase	probable esterase
alkaline serine pr	alkaline serine pr
hypothetical prote	hypothetical prote
K+ transport prote	K+ transport prote
glycerol-3-phospha	glycerol-3-phospha
xanthine/uracil pe	xanthine/uracil pe
hypothetical prote	hypothetical prote
IL2 protein - human	IL2 protein - human
hypothetical prote	hypothetical prote
hypothetical prote	hypothetical prote
probable membrane	probable membrane
probable amino aci	probable amino aci
conserved hypotet	conserved hypotet
hypothetical prote	hypothetical prote
L-lactate permease	L-lactate permease
proline permease (proline permease (
cell fusion glycop	cell fusion glycop
gene F protein - r	gene F protein - r
hypothetical prote	hypothetical prote
Rieske [2Fe-2S] ir	Rieske [2Fe-2S] ir
aplysinin A precu	aplysinin A precu
hypothetical prote	hypothetical prote
methyI-accepting c	methyI-accepting c
probable acyl-CoA	probable acyl-CoA
env polyprotein pr	env polyprotein pr
probable inositol	probable inositol
carbon starvation	carbon starvation
probable protein k	probable protein k
spingomyelin phos	spingomyelin phos
hypothetical prote	hypothetical prote
two-component sens	two-component sens

Db 1 MOEVLILLVLAGLPTLDANDP-ENKNDPFYYDMKSLRVGGLICAGILCALGIIVMSG 59
 Qy 60 KCKYKSQKQKSHSPVPEKAIPIITPGSATTC 89
 A:Reference number: A46435; MUID:93252993; PMID:8387529
 A:Accession: D46435
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-58 <MER>
 A:Cross-references: UNIPROT:Q04645; UNIPARC:UPI00001262A7; EMBL:X70059; NID:9396; PIDN:CT
 A:Note: the authors translated the codon TTC for residue 25 as Pro
 C:Keywords: hydrolase; transmembrane protein
 Db 60 KCKCKFRQKP-SHREGSPRLITPGSAHNC 88

RESULT 3
 A55571
 chloride conductance inducer Mat-8 - human
 C:Species: Homo sapiens (man)
 C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C:Accession: A55571
 R:Morrisson, B.W.; Moorman, J.R.; Kowdley, G.C.; Kobayashi, Y.M.; Jones, J.R.; Leder, P.
 J. Biol. Chem. 270, 2176-2182, 1995

A:Title: Mat-8, a novel phospholipase-like protein expressed in human breast tumors, ind
 A:Reference number: A55571; MUID:95138184; PMID:7836447
 A:Accession: A55571
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-87 <MOR>
 A:Cross-references: UNIPROT:Q14802; UNIPARC:UPI0000052765; GB:X93036; GB:S74645; NID:910
 C:Keywords: transmembrane protein
 Query Match 46.5%; Score 214.5; DB 2; Length 87;
 Best Local Similarity 54.5%; Pred. No. 1.2e-16;
 Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;

Qy 1 MERVTLALL-LAGLTALDPFANKDPPFYDMKNIQLSGTICGGTLATAGIAAVTSG 59
 Db 1 MOKVTGLGLVPLAGPVLDAND-LEDKNSPFYDWSLQVGLICAGVLCAMGIITVWSA 59

Qy 60 KCKYKSQKQK-HSPVPEKAIPIITPGSA 86
 Db 60 KCKCKFGQKSGHN--FGETPLITPGSA 85

RESULT 4
 A40533
 CAMP-dependent protein kinase major membrane substrate precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
 C:Accession: A40533
 R:Palmer, C.J.; Scott, B.T.; Jones, L.R.
 J. Biol. Chem. 266, 11126-11130, 1991
 A:Title: Purification and complete sequence determination of the major plasma membrane
 A:Reference number: A40533; MUID:91250422; PMID:1710217
 A:Accession: A40533
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-92 <PAL>
 A:Cross-references: UNIPROT:P56513; UNIPARC:UPI0000131C15; GB:M63934

Query Match 27.4%; Score 126.5; DB 2; Length 92;
 Best Local Similarity 41.4%; Pred. No. 7.1e-07;
 Matches 29; Conservative 15; Mismatches 23; Indels 3; Gaps 2;

Qy 8 LLLLAG-LTALDPFANKDPPFYDMKNIQLSGTICGGTLATAGIAAVTSGCKYSS 66
 Db 8 LVLGCGFLTTATKAP-QEHDPFYDYQSLRIGGLTAGILFIIIGLITVLSRRCKCFN 65

Qy 67 QKQSHPVPEK 76
 Db 66 QQQRTEGPDE 75

RESULT 5
 D46435
 Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C:Accession: D46435; S31525
 R:Mercer, R.W.; Biemederfer, D.; Blaes Jr., D.P.; Collins, J.H.; Forbush III, B.

J. Cell Biol. 121, 579-586, 1993
 A:Title: Molecular cloning and immunological characterization of the gamma polypeptide,
 A:Reference number: A46435; MUID:93252993; PMID:8387529
 A:Accession: D46435
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-58 <MER>
 A:Cross-references: UNIPROT:Q04645; UNIPARC:UPI00001262A7; EMBL:X70059; NID:9396; PIDN:CT
 A:Note: the authors translated the codon TTC for residue 25 as Pro
 C:Keywords: hydrolase; transmembrane protein

Query Match 20.9%; Score 96.5; DB 2; Length 58;
 Best Local Similarity 34.6%; Pred. No. 0.00092;
 Matches 19; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

Qy 27 DDPFYDMKNIQLSGTICGGTLATAGIAAVTSGCKYKSQKQKSHPVPEKAI 78
 Db 8 EDPFYDYETVRNGGLIFALAFIVGLVITLSKFRFC-GAKKHQRIPEDEL 58

RESULT 6
 A46435
 Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - sheep (fragment)
 N:Alternate names: sodium pump gamma chain; sodium/potassium-dependent ATPase gamma chain
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 22-Nov-1993 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C:Accession: A46435; S31524; A27383
 R:Mercer, R.W.; Biemederfer, D.; Blaes Jr., D.P.; Collins, J.H.; Forbush III, B.
 J. Cell Biol. 121, 579-586, 1993

A:Title: Molecular cloning and immunological characterization of the gamma polypeptide,
 A:Reference number: A46435; MUID:93252993; PMID:8387529
 A:Accession: A46435
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 6-53 <MER>

A:Cross-references: UNIPROT:Q04680; UNIPARC:UPI000017CC97
 A:Experimental source: kidney
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:131232, NCBI:P.131233)
 R:Mercer, R.W.
 submitted to the EMBL Data Library, December 1992

A:Description: Cloning and sequencing of gamma subunit of sodium potassium ATPase.
 A:Reference number: S31522
 A:Accession: S31524
 A:Molecule type: mRNA
 A:Residues: 6-19, 'F', '21-53 <MER>
 A:Cross-references: UNIPARC:UPI000016C4B7; EMBL:X70061; NID:91255; PIDN:CAA49665.1; PID:
 R:Collins, J.H.; Leese, J.
 Biochemistry 26, 8665-8668, 1987
 A:Title: The "gamma-subunit" of Na,K-ATPase: a small, amphiphilic protein with a unique
 A:Reference number: A27383; MUID:88163544; PMID:2831947
 A:Accession: A27383
 A:Molecule type: protein
 A:Residues: 1-19, 'F', '21-33 <COL>
 A:Cross-references: UNIPARC:UPI000017CC98
 C:Complex: heterotrimer; alpha, beta, and gamma chain
 C:Keywords: heterotrimer; hydrolase; transmembrane protein

Query Match 20.5%; Score 94.5; DB 2; Length 53;
 Best Local Similarity 34.6%; Pred. No. 0.0014;
 Matches 18; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

Qy 27 DDPFYDMKNIQLSGTICGGTLATAGIAAVTSGCKYKSQKQKSHPVPEKAI 78
 Db 3 EDPFYDYETVRNGGLIFALAFIVGLVITLSKFRFC-GAKKHQRIPEDEL 53

RESULT 7
 B46435
 Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C:Accession: B46435; S31523

R.Mercer, R.W.; Biemederfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.

J. Cell Biol. 121, 579-586, 1993

A:Title: Molecular cloning and immunological characterization of the gamma polypeptide,

A:Reference number: A6435; MUID:9325293; PMID:8387529

A:Accession: B6435

A:Status: preliminary

A:Molecule type: mRNA

A:Cross-references: UNIPROT:004679; UNIPARC:UPI0000170985; EMBL:X70062; NID:956299; PIDN

A:Note: the authors translated the codon TTC for residue 25 as Pro

C:Keywords: hydrolase; transmembrane protein

Query Match 16.4%; Score 75.5; DB 2; Length 58;

Best Local Similarity 34.7%; Pred. No. 0.19;

Matches 17; Conservative 12; Mismatches 19; Indels 1; Gaps 1;

Qy 27 DDFFYDMKNLQSLGICGLAIAVLSGCKKYSOKOHPVE 75

Db 8 ENPFYDIETVAKGGLIFAGLAFVVGILLISKRRFCGS-KKHQVNE 55

RESULT 8

Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

A:Accession: C46435; S1522

R:Mercer, R.W.; Biemederfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.

J. Cell Biol. 121, 579-586, 1993

A:Title: Molecular cloning and immunological characterization of the gamma polypeptide,

A:Reference number: A6435; MUID:9325293; PMID:8387529

A:Accession: C46435

A:Status: preliminary

A:Molecule type: mRNA

A:Cross-references: UNIPROT:004646; UNIPARC:UPI00001482CD; EMBL:X70060; NID:951111; PIDN

A:Note: the authors translated the codon TTC for residue 25 as Pro

C:Keywords: hydrolase; transmembrane protein

Query Match 15.9%; Score 73.5; DB 2; Length 58;

Best Local Similarity 32.7%; Pred. No. 0.32;

Matches 16; Conservative 12; Mismatches 20; Indels 1; Gaps 1;

Qy 27 DDFFYDMKNLQSLGICGLAIAVLSGCKKYSOKOHPVE 75

Db 8 ENPFYDIETVAKGGLIFAGLAFVVGILLISKRRFC-GGKHKQVNE 55

RESULT 9

plastoquinol-plastocyanin reductase (EC 1.10.99.1) 17K protein - Synechocystis sp. (sera

N:Alternate names: cytochrome b6-f complex chain IV; plastoquinol-plastocyanin reductase

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

A:Accession: A61088; S15474

R:Osiewacz, H.D.

Arch. Microbiol. 157, 336-342, 1992

A:Title: Construction of insertion mutants of Synechocystis sp. PCC 6803: evidence for a

A:Reference number: A61088; MUID:92272582; PMID:1590707

A:Accession: A61088

A:Molecule type: DNA

A:Residues: 1-160 <OSI>

A:Cross-references: UNIPROT:P27389; UNIPARC:UPI0000131690; EMBL:X58522; NID:947376; PIDN

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76298

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-160 <KAN>

A:Cross-references: UNIPARC:UPI0000131690; EMBL:D64000; GB:AB001339; NID:91001484; PIDN:

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Gene: petD

C:Superfamily: cytochrome b6-f complex, subunit 4 (plastoquinol-plastocyanin reductase,

C:Keywords: oxidoreductase; photosynthesis; thylakoid

F:24-144/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>

Query Match 15.6%; Score 72; DB 1; Length 160;

Best Local Similarity 37.7%; Pred. No. 1.4;

Matches 23; Conservative 9; Mismatches 21; Indels 8; Gaps 2;

Qy 7 ALLLAGLTAI-----EANDPANKD--PFYDMKNLQSLGICGLAIAVLS 58

Db 47 ALGULAGLAILDPMNIGSPADPFATPILDEWLYPFQRLIRLPNTLGIAGWAAIPL 106

Qy 59 G 59

Db 107 G 107

RESULT 10

conserved hypothetical protein ytcD - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

A:Accession: F69989

R:Kunst, F.; Ogata, N.; Moser, I.; Albertini, A.M.; Aloni, G.; Azevedo, V.; Berer

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gallier

tech, J.; Harwood, C.R.; Henauf, C.; Hilbert, H.; Holst, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel

Y. M.; Ogawa, K.; Ogilawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schoeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.F.; Zumein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: F69989

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-529 <KUN>

A:Cross-references: UNIPROT:O34355; UNIPARC:UPI0000608E4; GB:Z99119; GB:AL009126; NID:9

A:Experimental source: strain 168

C:Genetics:

A:Gene: ytcD

Query Match 15.4%; Score 71; DB 2; Length 529;

Best Local Similarity 30.4%; Pred. No. 6.2;

Matches 31; Conservative 9; Mismatches 24; Indels 38; Gaps 6;

Qy 16 ALBANDPANKDDPPYD-----WKNTLSGLICG-----LLAING 52

Db 381 ALDLPHPVASFPPVIRLKGDKRMKTAFAWTLISKGLICGSGSDADIPVDPILGIG- 439

Qy 53 IAAVSGCKYKSSOKOHP-----VP-EKAPILIPGSA 86

Db 440 -SAVLR-----KSHQNGPSYNESECLPYEALKLYEGSA 475

RESULT 11

probable membrane protein ypo3057 (imported) - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

A:Accession: AH0371

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchell, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A/Reference number: AB0001, MUID:21470413, PMID:11586360
A/Accession: AF0371
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-150 <KUR>
A/Cross-references: UNIPROT:Q8ZCD4, UNIPARC:UPI00000CD9C4, GB:AL590842, PIDN:CAC92299.1,
C/Genetics:
A/Gene: YPO3057
C/Superfamily: hypothetical protein ytwi

Query Match 15.0%; Score 69; DB 2; Length 150;
Best Local Similarity 30.2%; Pred. No. 2.7;
Matches 26; Conservative 14; Mismatches 32; Indels 14; Gaps 4;

Oy 4 VTLALLAGLTALANDPFANKDDPFYDWKNTQLSGLICGGLAIAGT-AAVLSGKCK 62
Db 26 VTLALLAGLTALANDPFANKDDPFYDWKNTQLSGLICGGLAIAGT-AAVLSGKCK 72
-----FFPW--VEKGLTITGVILITIGVWAPIASG--K 72

Oy 63 YKSQKOHSPYPERKAIPLITPGSAT 88
Db 73 ISASEVHSHFYQWKSILAIIVGVAVS 98

RESULT 12
A05009
hypothetical protein 135 - liverwort (Marchantia polymorpha) chloroplast
C/Species: chloroplast Marchantia polymorpha
C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C/Accession: S01571, A05009
R/Umesono, K.; Inokuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T
J. Mol. Biol. 203, 299-331, 1988
A/Title: Structure and organization of *Marchantia polymorpha* chloroplast genome. II. Gen
A/Reference number: S01567, MUID:8906866; PMID:2974083
A/Accession: S01571
A/Molecule type: DNA
A/Residues: 1-135 <UME>
A/Cross-references: UNIPROT:Q32616; UNIPARC:UPI000013A518; EMBL:X04465; NID:g11640; PIDN
R; Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi
Nature 322, 572-574, 1986
A/Title: Chloroplast gene organization deduced from complete sequence of liverwort March
A/Reference number: A38014
A/Contents: annotation; gene organization, sites, features
C/Genetics:
A/Genome: chloroplast
A/Intons: 36/1
C/Superfamily: hypothetical protein 135
C/Keywords: chloroplast

Query Match 14.6%; Score 67.5; DB 2; Length 135;
Best Local Similarity 33.6%; Pred. No. 3.6;
Matches 15; Conservative 11; Mismatches 13; Indels 7; Gaps 2;

Oy 9 LTLAANDPFANKDDPFYDWKNTQLSGLICGGLAIAG 52
Db 16 LTLAANDPFANKDDPFYDWKNTQLSGLICGGLAIAG 56
-----SCIGLICGGLIFPG 56

RESULT 13
B86620
cholesterol synthase [imported] - Chlamydia pneumoniae (strain J138)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: B86620
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A/Title: Comparison of whole genome sequences of *Chlamydia pneumoniae* J138.
A/Reference number: AB6491, MUID:20303049, PMID:10871362
A/Accession: B86620
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-359 <STO>
A/Cross-references: UNIPROT:Q9Z6M2, UNIPARC:UPI0000125F94, GB:BA000008, NID:g8979410, PII
A/Experimental source: strain J138
C/Genetics:
A/Gene: aroc
C/Superfamily: cholesterol synthase

Query Match 14.4%; Score 66.5; DB 2; Length 359;
Best Local Similarity 23.6%; Pred. No. 13;
Matches 25; Conservative 14; Mismatches 36; Indels 31; Gaps 4;

Oy 7 ALLIAGLTALANDPFANKD-----DPFYDWKNTQLSGLICGGLAIAGTAAVLSG 59
Db 234 ALMSIPAKFEGIKGASQMGSGYTDPFVWEGENITLKSNNCGGLTIGITGVPIEG 293
-----OHSP-VPERKAIPLI 81

Oy 60 KCKYK--SSOK-----OHSP-VPERKAIPLI 81
Db 294 RIAFKPTSSIKRPGCATVTKTKETTYRTPOTGRHDPVCAIRAVPVV 339
-----OHSP-VPERKAIPLI 81

RESULT 14
A72004
cholesterol synthase CP0815 [imported] - Chlamydia pneumoniae (strains CWL029 and AR3)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: A72004, D81536
R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A/Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.
A/Reference number: A72000, MUID:99206606; PMID:10192388
A/Accession: A72004
A/Molecule type: DNA
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-359 <ARN>
A/Cross-references: UNIPROT:Q9Z6M2; UNIPARC:UPI0000125F94; GB:AB001684; GB:AB001363; NID
A/Experimental source: strain CWL029
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of *Chlamydia trachomatis* MoPh and *Chlamydia pneumoniae* AR39.
A/Reference number: AB1500, MUID:20150255; PMID:10684935
A/Accession: D81536
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-359 <REA>
A/Cross-references: UNIPARC:UPI0000125F94; GB:AB002240; GB:AB002161; NID:g7189720; PIDN:
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Gene: aroc; CP0815
C/Superfamily: cholesterol synthase

Query Match 14.4%; Score 66.5; DB 2; Length 359;
Best Local Similarity 23.6%; Pred. No. 13;
Matches 25; Conservative 14; Mismatches 36; Indels 31; Gaps 4;

Oy 7 ALLIAGLTALANDPFANKD-----DPFYDWKNTQLSGLICGGLAIAGTAAVLSG 59
Db 234 ALMSIPAKFEGIKGASQMGSGYTDPFVWEGENITLKSNNCGGLTIGITGVPIEG 293
-----OHSP-VPERKAIPLI 81

Oy 60 KCKYK--SSOK-----OHSP-VPERKAIPLI 81
Db 294 RIAFKPTSSIKRPGCATVTKTKETTYRTPOTGRHDPVCAIRAVPVV 339
-----OHSP-VPERKAIPLI 81

RESULT 15
A38101
potassium channel KCNA3 - human
N/Alternate names: potassium channel HLK3; potassium channel PCN3; shaker-related potass
C/Species: Homo sapiens (hmn)
C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C/Accession: A38101, B38556; J52990
R/Altai, B.; Roney, G.; Honore, E.; Schmid-Alliana, A.; Matrei, M.G.; Leese, F.; Ricar

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OM protein - protein search, using sw model

Run on: December 14, 2005, 06:25:35 ; Search time 171 Seconds
(without alignments)
367.205 Million cell updates/sec

Title: US-10-063-557-50

Perfect score: 461
Sequence: 1 MERVTLALLAGLTALAN.....HSPVEKAIPIITPGSARTTC 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	89	2	Q6UWZ1 HUMAN
2	452	98.0	89	2	Q7Z4M5 HUMAN
3	450	97.6	88	1	FXVD4_HUMAN
4	276.5	60.0	88	1	FXVD4_MOUSE
5	256.5	55.6	87	1	FXVD4_RAT
6	244.5	52.4	88	1	FXVD3_MOUSE
7	234.5	50.9	88	1	FXVD3_RAT
8	230.5	50.0	88	1	FXVD3_MOUSE
9	214.5	46.5	87	1	FXVD3_PIG
10	214.5	46.5	87	2	Q6IB59_HUMAN
11	203	44.0	70	2	Q80UV3_MOUSE
12	129	28.0	92	1	PLM_HUMAN
13	127.5	27.7	88	2	Q4RFQ2_TETNG
14	126.5	27.4	92	1	PLM_CANFA
15	124.5	27.0	94	1	FXVD6_RAT
16	123.5	26.8	94	1	FXVD6_MOUSE
17	119	25.8	100	2	Q5M8E9_XENTR
18	116	25.2	94	2	Q70012_SQUAC
19	115.5	25.1	92	1	PLM_MOUSE
20	115	24.9	95	1	FXVD6_PONPY
21	113.5	24.6	95	2	Q6D7F4_XENLA
22	113	24.5	92	1	PLM_RAT
23	112.5	24.4	95	1	FXVD6_HUMAN
24	112.5	24.4	95	1	FXVD6_MACFA
25	110	23.9	95	2	Q5ZM59_CHICK
26	107.5	23.3	97	2	Q4RHT7_TETNG
27	103.5	22.5	94	2	Q6D7D6_XENLA
28	96.5	20.9	58	1	ATNG_BOVIN
29	96	20.8	99	2	Q7S252_BRARE
30	95.5	20.7	53	1	ATNG_SHEEP
31	95.5	20.7	65	2	Q58K79_PIG

32	94	20.4	178	1	FXVD5_HUMAN	Q96db9 homo sapien
33	92	20.0	178	1	FXVD5_RAT	P58647 ratius norv
34	92	20.0	178	2	Q6P9W0_RAT	Q6P9W0 ratius norv
35	89	19.3	80	1	FXVD7_HUMAN	P58549 homo sapien
36	85	18.4	80	1	FXVD7_MOUSE	P58648 mus musculu
37	84	18.2	178	1	Q8IWS1_HUMAN	Q8IWS1 homo sapien
38	83	18.0	66	1	ATNG_HUMAN	P54710 homo sapien
39	83	18.0	80	1	FXVD7_RAT	P58649 ratius norv
40	83	18.0	94	1	FXVD8_HUMAN	P58550 homo sapien
41	82.5	17.9	66	1	ATNG_RAT	Q04679 ratius norv
42	79.5	17.2	142	2	Q6P8R9_MOUSE	Q6P8R9 mus musculu
43	78	16.9	70	1	ATNG_MOUSE	Q04646 mus musculu
44	78	16.9	70	2	Q6IT12_MOUSE	Q6IT12 mus musculu
45	77.5	16.8	711	2	Q4NGJ7_PNICC	Q4NGJ7 athricobacte
46	76	16.5	289	2	Q4WU10_ASPIU	Q4WU10 aspergillus
47	75.5	16.4	524	2	Q5LOV1_SILPO	Q5LOV1 silicibacte
48	74	16.1	188	2	Q5LME5_SILPO	Q5LME5 silicibacte
49	74	16.1	208	2	Q4REB0_MACFA	Q4REB0 macaca fasc
50	73.5	15.9	64	2	Q6IT11_MOUSE	Q6IT11 mus musculu
51	73.5	15.9	82	2	Q6IT10_MOUSE	Q6IT10 mus musculu
52	73.5	15.9	196	2	Q9GZET_CAEEL	Q9GZET caenorhabdi
53	73.5	15.9	330	2	Q84EX9_ENTCL	Q84EX9 enterobacte
54	73.5	15.8	201	2	Q7OJ63_ANOGA	Q7J163 anophelle 9
55	73	15.8	455	2	Q4IPU0_GIBZV	Q4IPU0 gibbellella
56	73	15.8	1132	2	Q83861_PREOV	Q83861 niliaparvaca
57	72	15.8	1343	2	Q521Q6_MAGGR	Q521Q6 magnaporthe
58	72	15.6	160	1	PETD_SYNY3	P275189 synechocyst
59	71	15.4	61	1	ATNG_XENLA	Q13001 xenopus lae
60	71	15.4	529	2	Q34355_BACSU	Q34355 bacillus su
61	70.5	15.3	251	2	Q54F08_DICDI	Q54F08 dictyosteli
62	70.5	15.3	334	2	Q6D644_ERWCT	Q6D644 erwinta car
63	70	15.2	184	1	FXVD5_MOUSE	P97808 mus musculu
64	70	15.2	216	2	Q5ZFE6_PLAMJ	Q5ZFE6 plantago ma
65	69.5	15.1	236	2	Q6GME4_XENLA	Q6GME4 xenopus lae
66	68.5	15.1	268	2	Q4FSL8_PGNAM	Q4FSL8 psychrobact
67	68.5	15.1	458	2	Q5KUP7_GEOKA	Q5KUP7 geobactilli
68	69	15.0	150	2	Q8ZC04_YERPE	Q8ZC04 yerisinda pe
69	69	15.0	157	2	Q668G1_YERPE	Q668G1 yerisinda pe
70	69	15.0	150	2	Q8DOY1_YERPE	Q8DOY1 yerisinda pe
71	68.5	14.9	330	2	Q9IUK8_ARATH	Q9IUK8 arabidopsis
72	68.5	14.9	340	2	Q94E19_ARATH	Q94E19 arabidopsis
73	68.5	14.9	456	2	Q9CLJ0_PASMU	Q9CLJ0 pasteurrella
74	68.5	14.9	485	2	Q5BEK5_BRARE	Q5BEK5 brachydanto
75	68.5	14.9	499	2	Q5VHU4_CIOIN	Q5VHU4 ciona intes
76	68.5	14.9	531	2	Q5VHU5_CIOIN	Q5VHU5 ciona intes
77	68	14.8	173	2	Q8HKR3_PPERC	Q8HKR3 arcos sp. k
78	68	14.8	417	2	Q4QD23_LEIMA	Q4QD23 leishmania
79	68	14.8	978	2	Q6S9P5_ORYSA	Q6S9P5 oryza sativ
80	67.5	14.6	135	1	YCF66_MARPO	Q32616 marchantia
81	67.5	14.6	337	2	Q6L3V4_SOLDE	Q6L3V4 solanum dem
82	67.5	14.6	387	2	Q6YXY7_ORYSA	Q6YXY7 oryza sativ
83	67.5	14.6	664	2	Q75485_HUMAN	Q75485 homo sapien
84	67.5	14.6	664	2	Q8WU17_HUMAN	Q8WU17 homo sapien
85	67.5	14.6	664	2	Q5RBT7_PONPY	Q5RBT7 pongo pygma
86	67	14.5	364	1	Q5ZFS7_PLAMJ	Q5ZFS7 plantago ma
87	67	14.5	390	1	AROC_SILURO	Q96Y94 silulobus
88	67	14.5	715	2	Q72E54_DESVH	Q72E54 desulfovibr
89	66.5	14.4	198	2	Q51VA7_MAGGR	Q51VA7 magnaporthe
90	66.5	14.4	241	2	Q9K313_STRCO	Q9K313 streptomyce
91	66.5	14.4	329	2	Q6ODJ9_SOLUTU	Q6ODJ9 solanum tub
92	66.5	14.4	359	1	AROC_CHLPN	Q946M2 chlamydia p
93	66.5	14.4	516	2	Q28656_RABIT	Q28656 oryctolagus
94	66.5	14.4	523	1	KCNK33_HUMAN	P22001 homo sapien
95	66.5	14.4	546	2	Q5RA50_PONPY	Q5RA50 pongo pygma
96	66.5	14.4	549	2	Q8B9W6_SHEON	Q8B9W6 shewanella
97	66.5	14.4	557	2	Q6P2D3_HUMAN	Q6P2D3 homo sapien
98	66.5	14.4	575	2	Q5XWNO_HUMAN	Q5XWNO homo sapien
99	66	14.3	139	2	Q5XWNO_SOLUTU	Q5XWNO solanum tub
100	66	14.3	446	2	Q87UY7_SULISO	Q87UY7 sulfolobus
101	65.5	14.2	161	2	Q5ENJ3_CRYNE	Q5ENJ3 cryptococcu
102	65.5	14.2	161	2	Q5KBG5_CRYNE	Q5KBG5 cryptococcu
103	65.5	14.2	305	2	Q74DY6_GEOSL	Q74DY6 geobacter s
104	65.5	14.2	333	2	Q6L3P2_SOLDE	Q6L3P2 solanum dem

105	65.5	14.2	546	2	Q96N9_HUMAN	Q96n9 homo sapien	178	63	13.7	467	2	Q4ISE1_GIBZE	Q4ISE1 gibberella
106	65.5	14.2	546	2	Q86V42_HUMAN	Q86v42 homo sapien	179	63	13.7	468	2	Q9ZV47_ARATH	Q9Zv47 arabidopsis
107	65.5	14.2	582	2	Q8ABP9_HUMAN	Q8ABp9 homo sapien	180	63	13.7	466	2	Q7NBZ8_MYCGA	Q7NBz8 mycoplasma
108	65.5	14.2	1185	2	Q8EG58_SHEON	Q8EG58 shewanella	181	63	13.7	496	2	Q59QY3_CANAL	Q59Qy3 candida alb
109	65.5	14.2	1278	2	Q4SM9C_TETNG	Q4SM9C tetradon n	182	63	13.7	622	2	Q8KWT9_STRPU	Q8KWT9 streptococ
110	65	14.1	1344	2	Q8R157_BRARE	Q8R157 brachydanio	183	63	13.7	655	2	Q8DUN3_STRPU	Q8DUN3 streptococ
111	65	14.1	327	2	Q9LVG3_ARATH	Q9LVg3 arabidopsis	184	63	13.7	750	2	Q59R09_CANAL	Q59R09 candida alb
112	65	14.1	427	2	Q9LV91_THEAN	Q9LV91 theilleria a	185	63	13.7	808	2	Q6DDP6_XENLA	Q6DDp6 xenopus lae
113	65	14.1	469	2	Q9XDX1_MAGMG	Q9XDX1 magnetospir	186	63	13.7	825	2	Q99JG5_9GAMA	Q99JG5 gallitrichi
114	65	14.1	582	2	Q5UQ22_MIMIV	Q5Uq22 mimivirina	187	63	13.7	912	2	Q8D4M3_VIBVA	Q8D4M3 vibrio vuln
115	65	14.1	760	2	Q90638_CHICK	Q90638 gallus gall	188	63	13.7	923	2	Q5B8X2_VIBF1	Q5B8X2 vibrio fisc
116	65	14.1	832	2	Q4SB80_TETNG	Q4SB80 tetradon n	189	63	13.7	927	2	Q9N389_CAEEL	Q9N389 caenorhabd
117	64.5	14.0	155	2	Q9R126_MOUSE	Q9R126 mus musculu	190	63	13.7	1022	2	Q27779_SCHNA	Q27779 schistosoma
118	64.5	14.0	189	2	Q6C1N8_YARLI	Q6C1n8 yarrowia l1	191	63	13.7	1411	2	Q5AS38_EMEH1	Q5AS38 aspergillus
119	64.5	14.0	244	2	Q7ZEX5_DESVH	Q7ZEX5 deulfovibr	192	62.5	13.6	146	2	Q81GV1_BACCR	Q81GV1 bacillus ce
120	64.5	14.0	311	2	Q4HB57_PDEIO	Q4hb57 rhodococcus	193	62.5	13.6	160	2	Q8PFE0_SCHJA	Q8PFE0 schistosoma
121	64.5	14.0	312	2	Q7YIY2_LISMP	Q7YIY2 listeria mo	194	62.5	13.6	163	2	Q73CB6_SCHJA	Q73CB6 bacillus ce
122	64.5	14.0	372	2	Q5MW34_LEGPL	Q5MW34 legionella	195	62.5	13.6	207	2	Q8TBL6_HUMAN	Q8TBL6 homo sapien
123	64.5	14.0	452	2	Q7T165_BRARE	Q7T165 brachydanio	196	62.5	13.6	286	2	Q9BSB3_HUMAN	Q9BSb3 homo sapien
124	64.5	14.0	455	2	Q8TXZ5_PYRFU	Q8TXz5 pyrococcus	197	62.5	13.6	299	1	COMO_BACSU	COMO bacillus su
125	64.5	14.0	465	2	Q86O80_RHOSH	Q86O80 rhodobacter	198	62.5	13.6	303	2	Q9UNZ3_HUMAN	Q9UNZ3 homo sapien
126	64.5	14.0	550	2	Q9QEW7_PPAPA	Q9QEW7 measles vir	199	62.5	13.6	339	2	Q53HB8_HUMAN	Q53HB8 homo sapien
127	64.5	14.0	550	2	Q9QEW9_PPAPA	Q9QEW9 measles vir	200	62.5	13.6	339	2	Q96BY9_HUMAN	Q96BY9 homo sapien
128	64.5	14.0	633	2	Q4SHG0_TETNG	Q4SHG0 tetradon n	201	62.5	13.6	339	2	Q9Y6B3_HUMAN	Q9Y6B3 homo sapien
129	64.5	14.0	677	2	Q5GU05_XANOR	Q5GU05 xanthomonas	202	62.5	13.6	372	2	Q5ZUV1_LEGPH	Q5ZUV1 legionella
130	64.5	14.0	725	2	Q8AY05_DROME	Q8AY05 drosophila	203	62.5	13.6	434	2	Q6HHZ7_BACHK	Q6HHz7 bacillus ch
131	64.5	14.0	871	2	Q5A4X3_CANAL	Q5A4X3 candida alb	204	62.5	13.6	434	2	Q81PF7_BACAN	Q81PF7 bacillus an
132	64.5	14.0	920	2	Q6XR97_P9ACT	Q6XR97 uncultured	205	62.5	13.6	492	2	Q750E3_ASHGO	Q750E3 ashyba gose
133	64.5	14.0	1750	2	Q4WRV3_ASPTU	Q4WRV3 aspergillus	206	62.5	13.6	504	2	Q7S9U0_NEUCR	Q7S9U0 neurospora
134	64	13.9	186	2	Q4RH15_TETNG	Q4RH15 tetradon n	207	62.5	13.6	525	2	Q76Z35_TRYCO	Q76Z35 trypanosoma
135	64	13.9	250	2	Q7WU64_9THEM	Q7WU64 thermotoga	208	62.5	13.6	525	2	Q9NC29_TRYCO	Q9NC29 trypanosoma
136	64	13.9	303	2	Q4KGC4_PSEBF5	Q4KGC4 pseudomonas	209	62.5	13.6	539	2	Q9RD59_STRCO	Q9RD59 streptomyce
137	64	13.9	315	2	Q9LSS8_ARATH	Q9LSS8 arabidopsis	210	62.5	13.6	557	2	Q7XQW8_ORYSA	Q7XQW8 oryza sativ
138	64	13.9	340	2	Q7ZM35_LEPIC	Q7ZM35 leptospira	211	62.5	13.6	580	2	Q5T6S3_HUMAN	Q5T6S3 homo sapien
139	64	13.9	383	2	Q6R5J0_RHORA	Q6R5J0 rhodopseudo	212	62.5	13.6	604	2	Q6N038_HUMAN	Q6N038 homo sapien
140	64	13.9	436	2	Q86VR7_HUMAN	Q86VR7 homo sapien	213	62.5	13.6	621	2	Q72PX8_LEPIC	Q72PX8 leptospira
141	64	13.9	525	1	KCNV3_RAT	P13384 rattus norv	214	62.5	13.6	663	2	Q8F647_LEPIN	Q8F647 leptospira
142	64	13.9	582	2	Q6K620_ORYSA	Q6K620 oryza sativ	215	62.5	13.6	663	2	Q8QSL5_TETNG	Q8QSL5 tetradon n
143	64	13.9	678	2	Q9BJM1_TRISP	Q9BJM1 trichinella	216	62.5	13.6	670	2	Q4SQ15_TETNG	Q4SQ15 tetradon n
144	64	13.9	678	2	Q8R9G1_THETN	Q8R9G1 theomaner	217	62.5	13.6	685	2	Q8EBZ6_SHEON	Q8EBZ6 shewanella
145	64	13.9	727	2	Q6F1K3_CANCA	Q6F1K3 candida gla	218	62.5	13.6	700	2	Q8TGO0_ASPTU	Q8TGO0 aspergillus
146	64	13.9	804	2	Q75GV0_ORYSA	Q75GV0 oryza sativ	219	62.5	13.6	700	2	Q4WSB9_ASPTU	Q4WSB9 aspergillus
147	64	13.9	915	2	Q7MG71_VIBVY	Q7MG71 vibrio vuln	220	62.5	13.6	760	2	Q7XNUS_ORYSA	Q7XNUS oryza sativ
148	64	13.9	1046	2	Q82MK5_NITEU	Q82MK5 nitrobomona	221	62.5	13.6	769	1	KCNK3_ORYSA	KCNK3 mus musculu
149	63.5	13.8	241	2	Q8UX90_HALMA	Q8UX90 haloarcula	222	62.5	13.6	850	2	Q6SMY9_BACLD	Q6SMY9 bacillus l1
150	63.5	13.8	309	2	Q8Y5P7_LISMO	Q8Y5P7 listeria mo	223	62.5	13.6	910	1	SYL_NEIMA	SYL neisseria m
151	63.5	13.8	309	2	Q9ZAO5_LISIN	Q9ZAO5 listeria in	224	62.5	13.6	1048	1	SIL_SALTY	SIL salaria
152	63.5	13.8	318	2	Q4TG61_GIBZE	Q4TG61 gibberella	225	62.5	13.6	1048	2	Q6MXQ0_SERMA	Q6MXQ0 sericia ma
153	63.5	13.8	327	2	Q6ZVM5_HUMAN	Q6ZVM5 homo sapien	226	62	13.4	150	2	Q89JN4_CLOTE	Q89JN4 clostridium
154	63.5	13.8	359	2	Q8Z2F8_CHICV	Q8Z2F8 chlamydomo	227	62	13.4	179	1	DSBB_HABDU	DSBB haemophilus
155	63.5	13.8	372	2	Q5X4P4_LEGPA	Q5X4P4 legionella	228	62	13.4	189	2	Q6X9L3_SULIS	Q6X9L3 sulfolobus
156	63.5	13.8	396	2	Q5UUL7_9PEZI	Q5UUL7 cercophora	229	62	13.4	269	2	Q6YWM5_ORYSA	Q6YWM5 oryza sativ
157	63.5	13.8	410	2	Q4LUU0_9BURK	Q4LUU0 burkholderi	230	62	13.4	308	2	Q61BX8_CABER	Q61BX8 caenorhabd
158	63.5	13.8	420	2	Q61568_ORYSA	Q61568 oryza sativ	231	62	13.4	308	2	Q8BRU1_MOUSE	Q8BRU1 mouse
159	63.5	13.8	452	2	Q6FVH0_CANCA	Q6FVH0 candida gla	232	62	13.4	381	2	Q8UC07_AGRIS	Q8UC07 agrobacteri
160	63.5	13.8	511	1	KCNK1_HUMAN	P48547 homo sapien	233	62	13.4	393	2	Q7CMG7_AGRIS	Q7CMG7 agrobacteri
161	63.5	13.8	511	1	KCNK1_MOUSE	P15388 mus musculu	234	62	13.4	414	2	Q323B3_STRGR	Q323B3 streptomyce
162	63.5	13.8	511	2	Q5BN35_RABIT	Q5BN35 cryptocolagus	235	62	13.4	419	2	Q7XTD2_ORYSA	Q7XTD2 oryza sativ
163	63.5	13.8	511	2	Q5BN36_BOVIN	Q5BN36 bos taurus	236	62	13.4	445	2	Q96X94_SULTO	Q96X94 sulfobus
164	63.5	13.8	521	2	Q4V7K2_XENLA	Q4V7K2 xenopus lae	237	62	13.4	470	2	Q8PHR1_XANNC	Q8PHR1 xanthomonas
165	63.5	13.8	550	2	Q9QEW8_PPAPA	Q9QEW8 measles vir	238	62	13.4	489	2	Q65UC0_NANSM	Q65UC0 nanaimia
166	63.5	13.8	585	1	KCNK1_RAT	P25122 rattus norv	239	62	13.4	558	2	Q8N1V9_HUMAN	Q8N1V9 homo sapien
167	63.5	13.8	585	2	Q9X5J8_CANFA	Q9X5J8 canis faml1	240	62	13.4	577	2	Q9V7C4_DROME	Q9V7C4 drosophila
168	63.5	13.8	620	2	Q7U2A5_MYCBO	Q7U2A5 mycobacteri	241	62	13.4	581	1	FUR4_SCHPO	FUR4 schistosach
169	63.5	13.8	620	2	Q07239_MYCTU	Q07239 mycobacteri	242	62	13.4	613	2	Q96P50_HUMAN	Q96P50 homo sapien
170	63.5	13.8	642	2	Q4SZN6_TETNG	Q4SZN6 tetradon n	243	62	13.4	629	2	Q86R09_HUMAN	Q86R09 homo sapien
171	63.5	13.8	725	2	Q5HL36_CANLA	Q5HL36 campylobact	244	62	13.4	631	2	Q96PR1_HUMAN	Q96PR1 homo sapien
172	63.5	13.8	747	2	Q575Z7_MAIZE	Q575Z7 zea mays (m	245	62	13.4	648	2	Q4LB77_HUMAN	Q4LB77 homo sapien
173	63	13.7	125	2	Q7UJ33_CHRVO	Q7UJ33 chromobacte	246	62	13.4	777	2	Q51502_PSEAE	Q51502 pseudomonas
174	63	13.7	201	2	Q5N5M0_SYND6	Q5N5M0 synechococc	247	62	13.4	862	2	Q6MYC9_ASPTU	Q6MYC9 aspergillus
175	63	13.7	201	2	Q5N5M0_SYND6	Q5N5M0 synechococc	248	62	13.4	862	2	Q4WS99_ASPTU	Q4WS99 aspergillus
176	63	13.7	378	2	Q70FG1_ANOGA	Q70FG1 anopheles g	249	62	13.4	962	2	Q6BZ68_DBBHA	Q6BZ68 debaryomyce
177	63	13.7	465	2	Q4PDK1_USTMA	Q4PDK1 ustilago ma	250	62	13.4	1025	2	Q4QGS8_LEIMA	Q4QGS8 leishmania

251	62	13.4	1057	2	Q6FT12_CANGA	Q6FT12 candida gla	324	61	13.2	413	2	Q59KD6_CANAL	Q59KD6 candida alb
252	62	13.3	2325	2	Q6N3X8_CABEL	Q6N3X8 caenorhabdi	325	61	13.2	461	2	Q6SSP6_ECOLI	Q6SSP6 escherichia
253	61.5	13.3	134	2	Q6RSM0_9BACI	Q6RSM0 bacillus sp	326	61	13.2	461	2	Q7ACQ0_ECO57	Q7ACQ0 escherichia
254	61.5	13.3	178	2	Q63E78_COXBU	Q63E78 coxiella bu	327	61	13.2	463	2	Q6VIR1_PYRAB	Q6VIR1 pyrococcus
255	61.5	13.3	180	2	Q6T5E4_COXSA	Q6T5E4 coxysa	328	61	13.2	463	2	Q59471_PYRHO	Q59471 pyrococcus
256	61.5	13.3	206	2	Q5UELE_PYRKO	Q5UELE pyroko	329	61	13.2	463	2	Q6S337_ECOLI	Q6S337 escherichia
257	61.5	13.3	210	2	Q636E4_BACCZ	Q636E4 bacillus ce	330	61	13.2	464	2	Q7DBF2_ECO57	Q7DBF2 escherichia
258	61.5	13.3	213	2	Q6RFR7_CORBF	Q6RFR7 corynbacte	331	61	13.2	484	2	Q5GXA1_XANOR	Q5GXA1 xanthomonas
259	61.5	13.3	216	2	Q4N3J0_9M1CC	Q4N3J0 archibacte	332	61	13.2	488	2	Q5Z1J6_NOCFA	Q5Z1J6 nocardia fa
260	61.5	13.3	216	2	Q7V8X4_PROMM	Q7V8X4 prochloroc	333	61	13.2	502	2	Q5DAP6_SCHJA	Q5DAP6 schistosoma
261	61.5	13.3	260	2	Q6R9N10_BRAJA	Q6R9N10 bradyrhizob	334	61	13.2	520	2	Q5SHZ3_ARATH	Q5SHZ3 arabidopsis
262	61.5	13.3	262	2	Q6N8Y1_AGRIP	Q6N8Y1 agrotis ips	335	61	13.2	542	2	Q5YVGO_NOCFA	Q5YVGO nocardia fa
263	61.5	13.3	301	2	Q5SKX5_CRYNE	Q5SKX5 cryptococcu	336	61	13.2	568	2	Q61FR3_CABER	Q61FR3 caenorhabdi
264	61.5	13.3	303	2	Q5KAK4_CRYNE	Q5KAK4 cryptococcu	337	61	13.2	638	2	Q6MLY6_BDEBA	Q6MLY6 bellevibri
265	61.5	13.3	303	2	Q5R491_PONPY	Q5R491 pongo pygma	338	61	13.2	651	2	Q6DDN7_9TELE	Q6DDN7 apteronotus
266	61.5	13.3	320	2	Q6LRF1_PHOPR	Q6LRF1 photobacter	339	61	13.2	653	2	Q73T88_WYCPA	Q73T88 mycobacteri
267	61.5	13.3	327	2	Q6MX9_BDEBA	Q6MX9 bellevibri	340	61	13.2	1305	1	TCGAP_MOUSE	TCGAP mus musculu
268	61.5	13.3	342	1	ISTA_SYNY3	Q55274 synecocyst	341	61	13.2	1526	2	Q5K7V4_CRYNE	Q5K7V4 cryptococcu
269	61.5	13.3	347	2	Q6R1Z2_MOUSE	Q6R1Z2 mus musculu	342	61	13.2	1866	2	Q51IB7_CRYNE	Q51IB7 streptococ
270	61.5	13.3	381	2	Q6R1V9_LACPL	Q6R1V9 lactobacill	343	60.5	13.1	163	2	Q62HN5_STRAW	Q62HN5 anaeoromyxob
271	61.5	13.3	382	2	Q4Q9N5_LEIMA	Q4Q9N5 leishmania	344	60.5	13.1	176	2	Q5GYF6_XANOR	Q5GYF6 xanthomonas
272	61.5	13.3	399	2	Q6R9M3_BRAJA	Q6R9M3 bradyrhizob	345	60.5	13.1	210	1	Q5VJPI_DROME	Q5VJPI drosophila
273	61.5	13.3	427	2	Q5WKB5_BACSK	Q5WKB5 bacillus ci	346	60.5	13.1	210	1	PYRE_BACCI	PYRE bacilli an
274	61.5	13.3	433	2	Q5K1T7_CHLPN	Q5K1T7 chlamydia p	347	60.5	13.1	210	1	PYRE_BACCR	PYRE bacilli ce
275	61.5	13.3	433	2	Q5K1T7_CHLPN	Q5K1T7 chlamydia p	348	60.5	13.1	210	1	PYRE_BACCR	PYRE bacilli th
276	61.5	13.3	433	2	Q5K1T7_CHLPN	Q5K1T7 chlamydia p	349	60.5	13.1	210	1	Q4M7J6_BACCE	Q4M7J6 bacillus th
277	61.5	13.3	434	2	Q736Y4_BACCI	Q736Y4 bacillus ce	350	60.5	13.1	210	2	Q6R9X0_ARATH	Q6R9X0 arabidopsis
278	61.5	13.3	437	2	Q6RPF5_HUMAN	Q6RPF5 homo sapien	351	60.5	13.1	227	2	Q6R741_9NEOP	Q6R741 pediculus h
279	61.5	13.3	445	2	Q5T1J3_SALCH	Q5T1J3 salmoneila	352	60.5	13.1	253	2	Q6R741_9NEOP	Q6R741 pediculus h
280	61.5	13.3	445	2	Q5PKR4_SALPA	Q5PKR4 salmoneila	353	60.5	13.1	289	2	Q7S921_NEUCR	Q7S921 neurospora
281	61.5	13.3	445	2	Q6Z2L3_SALTI	Q6Z2L3 salmoneila	354	60.5	13.1	295	2	Q6Z2B8_ARATH	Q6Z2B8 arabidopsis
282	61.5	13.3	445	2	Q6Z2L3_SALTI	Q6Z2L3 salmoneila	355	60.5	13.1	306	2	Q4NYU8_9DELTA	Q4NYU8 anaeoromyxob
283	61.5	13.3	458	2	Q6D860_BRMC1	Q6D860 bruxia car	356	60.5	13.1	312	2	Q5KXES_BACHD	Q5KXES bacillus ha
284	61.5	13.3	461	2	Q4FPN8_9LITI	Q4FPN8 leisteria iv	357	60.5	13.1	319	2	Q4YCE8_PLABE	Q4YCE8 plasmodium
285	61.5	13.3	495	2	Q4SRQ6_TETNG	Q4SRQ6 tetraodon n	358	60.5	13.1	326	2	Q5Y7M6_SUTISO	Q5Y7M6 sulfolobus
286	61.5	13.3	522	2	Q64D05_LISIV	Q64D05 listeria iv	359	60.5	13.1	327	2	Q5XWRO_SOLTU	Q5XWRO solanum tub
287	61.5	13.3	523	2	Q64D04_LISIV	Q64D04 listeria iv	360	60.5	13.1	340	2	Q6LAAZ_ARATH	Q6LAAZ arabidopsis
288	61.5	13.3	524	1	P60_LISIV	Q61837 listeria iv	361	60.5	13.1	354	2	Q5M9T5_ARATH	Q5M9T5 arabidopsis
289	61.5	13.3	545	2	Q5QEW6_9PARA	Q5QEW6 megalos vir	362	60.5	13.1	427	2	Q5A315_CAVCR	Q5A315 caulobacter
290	61.5	13.3	549	2	Q5Y3U6_DROME	Q5Y3U6 drosophila	363	60.5	13.1	434	2	Q4MG72_BACCE	Q4MG72 bacillus ce
291	61.5	13.3	566	2	Q73L70_TREDE	Q73L70 treponema d	364	60.5	13.1	434	2	Q63AK9_BACCZ	Q63AK9 bacillus ce
292	61.5	13.3	592	2	Q6PVD1_XENLA	Q6PVD1 xenopus lae	365	60.5	13.1	463	2	Q61CUS_BACCR	Q61CUS bacillus ce
293	61.5	13.3	668	2	Q6R8Z0_MOUSE	Q6R8Z0 mus musculu	366	60.5	13.1	463	2	Q6B167_YERPE	Q6B167 yersinia pe
294	61.5	13.3	668	2	Q7TMV1_MOUSE	Q7TMV1 mus musculu	367	60.5	13.1	463	2	Q6EDX2_YERPE	Q6EDX2 yersinia ps
295	61.5	13.3	701	2	Q4G019_HUMAN	Q4G019 homo sapien	368	60.5	13.1	463	2	Q6R8C2_YERPE	Q6R8C2 yersinia pe
296	61.5	13.3	746	2	Q51KR6_MACGR	Q51KR6 magnaporthe	369	60.5	13.1	474	2	Q63187_BURPS	Q63187 burkholderi
297	61.5	13.3	805	2	Q62L28_BURMA	Q62L28 burkholderi	370	60.5	13.1	478	2	Q5YK87_DROME	Q5YK87 drosophila
298	61.5	13.3	831	2	Q60XB5_CABER	Q60XB5 caenorhabdi	371	60.5	13.1	484	2	Q6R861_9CAUD	Q6R861 bacterioph
299	61.5	13.3	855	2	Q63T81_BURPS	Q63T81 burkholderi	372	60.5	13.1	484	2	Q4ZBP3_9VIRU	Q4ZBP3 bacterioph
300	61.5	13.3	977	2	Q6R6RD9_HUMAN	Q6R6RD9 homo sapien	373	60.5	13.1	516	2	Q4ZDK0_9VIRU	Q4ZDK0 bacterioph
301	61.5	13.3	977	2	Q5YVK9_HUMAN	Q5YVK9 homo sapien	374	60.5	13.1	516	2	Q5M174_ARATH	Q5M174 arabidopsis
302	61.5	13.3	990	2	Q6Q4G3_HUMAN	Q6Q4G3 homo sapien	375	60.5	13.1	547	2	Q4R401_MACFA	Q4R401 macaca fasc
303	61.5	13.3	1145	2	Q6GUE7_9LILI	Q6GUE7 cynodoea n	376	60.5	13.1	560	2	Q5E1A5_AZOSE	Q5E1A5 azarocetes sp
304	61.5	13.3	1222	2	Q5AL53_CANAL	Q5AL53 candida alb	377	60.5	13.1	618	2	Q5G6W9_9POAL	Q5G6W9 carex backi
305	61.5	13.3	1499	2	Q8YK83_ANASP	Q8YK83 anabaena sp	378	60.5	13.1	638	1	Q5G6W9_9POAL	P22462 rattus norv
306	61.5	13.2	100	2	Q6VEB3_PSESY	Q6VEB3 pseudomonas	379	60.5	13.1	658	2	Q7VBR1_PROMM	Q7VBR1 prochloroc
307	61	13.2	139	2	Q6R7H7_VIRBA	Q6R7H7 vibrio para	380	60.5	13.1	726	2	Q4HSU4_CAMUP	Q4HSU4 campylobact
308	61	13.2	157	2	Q6BVI7_STIRU	Q6BVI7 streptococ	381	60.5	13.1	728	1	PURL_CAMUR	PURL campylobact
309	61	13.2	173	2	Q7Q505_ANOGA	Q7Q505 anopheles g	382	60.5	13.1	728	1	Q4H1H9_CAMCO	Q4H1H9 campylobact
310	61	13.2	173	2	Q6M722_SERMA	Q6M722 serratia ma	383	60.5	13.1	742	2	Q5Q0S7_9INFA	Q5Q0S7 influenza a
311	61	13.2	180	2	Q6L1G6_MOUSE	Q6L1G6 mus musculu	384	60.5	13.1	776	2	Q7NT42_CHRVO	Q7NT42 chromobact
312	61	13.2	187	2	Q5H2U1_XENTR	Q5H2U1 xenopus tro	385	60.5	13.1	917	2	Q7SV17_STRAWA	Q7SV17 streptococ
313	61	13.2	238	2	Q5V6G2_HALMA	Q5V6G2 halorcula	386	60.5	13.1	917	2	Q7RPM7_ANOGA	Q7RPM7 anopheles g
314	61	13.2	268	2	Q5A859_CAVCR	Q5A859 caulobacter	387	60.5	13.1	1038	2	Q4TUI7_AZOV1	Q4TUI7 azotobacter
315	61	13.2	272	2	Q6G9V3_ECOLI	Q6G9V3 escherichia	388	60.5	13.1	1155	2	Q51S12_9REOV	Q51S12 avian ortho
316	61	13.2	302	2	Q54880_RAT	Q54880 rattus norv	389	60.5	13.1	1285	2	Q51S13_9REOV	Q51S13 avian ortho
317	61	13.2	326	2	Q34086_COCER	Q34086 coccyzus er	390	60.5	13.1	1285	2	Q51S14_9REOV	Q51S14 avian ortho
318	61	13.2	326	2	Q762D5_MOUSE	Q762D5 mus musculu	391	60.5	13.1	1285	2	Q51S15_9REOV	Q51S15 avian ortho
319	61	13.2	338	1	IGT_TREDE	P60974 treponema d	392	60.5	13.1	1285	2	Q51S16_9REOV	Q51S16 avian ortho
320	61	13.2	355	2	Q5S592_COTJA	Q5S592 coturnix co	393	60.5	13.1	1285	2	Q51S17_9REOV	Q51S17 avian ortho
321	61	13.2	380	2	Q7P649_ANOGA	Q7P649 anopheles g	394	60.5	13.1	1285	2	Q51S18_9REOV	Q51S18 avian ortho
322	61	13.2	389	2	Q7T197_CHICK	Q7T197 gallus gall	395	60.5	13.1	1285	2	Q51S19_9REOV	Q51S19 avian ortho
323	61	13.2	395	2	Q588F9_RHILCO	Q588F9 rhizobium 1	396	60.5	13.1	1285	2		

397	60.5	13.1	1285	2	Q6JUV1_9REOV	Q6JUV1 avian recvi	470	59.5	12.9	579	2	Q5GTF9_WOLTR	Q5GTF9 wolbachia s
398	60.5	13.1	1319	2	Q5AYC8_EMENTI	Q5AYC8 aspergillus	471	59.5	12.9	579	2	Q73166_WOLPM	Q73166 wolbachia p
399	60.5	13.1	1748	2	Q9HGZ5_ASPOR	Q9HGZ5 aspergillus	472	59.5	12.9	624	2	Q55X46_CRYNE	Q55X46 cryptococcus
400	60	13.0	71	1	VITB1_XENIA	P1010 xenopus lae	473	59.5	12.9	624	2	Q5KMT6_CRYNE	Q5KMT6 cryptococcus
401	60	13.0	165	2	Q8BEP3_OCEIH	Q8BEP3 oceanobacti	474	59.5	12.9	636	2	Q4ZNR6_PSESY	Q4ZNR6 pseudomonas
402	60	13.0	218	2	Q6LTC3_PHOPR	Q6LTC3 photobacter	475	59.5	12.9	636	2	Q87ZAB_PSESY	Q87ZAB pseudomonas
403	60	13.0	249	2	Q8MM93_BRARE	Q8MM93 brachydanio	476	59.5	12.9	677	2	Q98TW3_XENIA	Q98TW3 xenopus lae
404	60	13.0	269	2	Q8YXAO_ANAPR	Q8YXAO anabaena sp	477	59.5	12.9	715	2	Q8PSH8_METWA	Q8PSH8 methanobact
405	60	13.0	275	2	Q9VLF6_DROME	Q9VLF6 drosophila	478	59.5	12.9	735	2	Q5E3S0_VIBFL	Q5E3S0 vibrio flac
406	60	13.0	288	2	Q8B1QO_PSEPK	Q8B1QO pseudomonas	479	59.5	12.9	778	2	Q4RVZ3_TETNG	Q4RVZ3 tetradon n
407	60	13.0	316	2	Q9VYV1_DROME	Q9VYV1 drosophila	480	59.5	12.9	841	2	Q8H1O5_ARATH	Q8H1O5 arabidopsis
408	60	13.0	324	2	Q986J3_RHIO	Q986J3 rhizobium l	481	59.5	12.9	841	2	Q8RWY4_ARATH	Q8RWY4 arabidopsis
409	60	13.0	325	2	Q7XMP8_ORYSA	Q7XMP8 oryza sativ	482	59.5	12.9	847	2	Q9SGW2_ARATH	Q9SGW2 arabidopsis
410	60	13.0	341	1	PAX9_HUMAN	P55771 homo sapien	483	59.5	12.9	894	2	Q8T043_DROME	Q8T043 drosophila
411	60	13.0	342	1	PAX9_MOUSE	P47242 mus musculu	484	59.5	12.9	1037	2	Q9VZS3_DROME	Q9VZS3 drosophila
412	60	13.0	342	2	Q8BSB1_MOUSE	Q8BSB1 mus musculu	485	59.5	12.9	1048	2	Q4NQ40_9DELT	Q4NQ40 9delu
413	60	13.0	352	2	Q5DMS5_KARMI	Q5DMS5 karlodinum	486	59.5	12.9	1138	2	Q12371_VITUR	Q12371 vitru
414	60	13.0	365	2	Q69135_9GAMA	Q69135 human herpe	487	59.5	12.9	1800	2	Q81RP5_DICDI	Q81RP5 dictyostei
415	60	13.0	369	2	Q6D4F3_ERWCT	Q6D4F3 erwinta car	488	59.5	12.9	1800	2	Q54PVL_DICDI	Q54PVL dictyostei
416	60	13.0	378	2	Q8AZK9_9GAMA	Q8AZK9 human herpe	489	59.5	12.8	119	2	Q9GMZ2_PIG	Q9GMZ2 pig
417	60	13.0	412	2	Q913M4_PSEAE	Q913M4 pseudomonas	490	59	12.8	130	2	Q8XBD8_ECOS7	Q8XBD8 ecoc
418	60	13.0	497	1	LMP2_EBV	P13285 Epstein-Bar	491	59	12.8	149	2	Q8HUG2_LACPL	Q8HUG2 lactobacill
419	60	13.0	497	2	Q777H4_9GAMA	Q777H4 human herpe	492	59	12.8	150	2	Q6D7R0_ERMCT	Q6D7R0 ermct
420	60	13.0	502	2	Q9BGM9_9GAMA	Q9BGM9 teahygiolusu	493	59	12.8	155	2	Q923L7_MOUSE	Q923L7 mouse
421	60	13.0	518	2	Q9XEO1_STRVG	Q9XEO1 streptomyc	494	59	12.8	167	2	Q8W9B3_VOMUR	Q8W9B3 vomur
422	60	13.0	519	2	Q82LO9_STRAM	Q82LO9 streptomyc	495	59	12.8	169	2	Q744R5_MYCPA	Q744R5 mycobact
423	60	13.0	524	2	Q71198_CHICK	Q71198 gallus gall	496	59	12.8	175	2	Q79713_FALPE	Q79713 falco peregr
424	60	13.0	525	2	Q83J01_SHIFL	Q83J01 shigella fl	497	59	12.8	177	2	Q92AM4_LISIN	Q92AM4 lisin
425	60	13.0	538	1	Y1EC_ECOLI	P26218 escherichia	498	59	12.8	189	2	Q6XK8_SULTS	Q6XK8 sulfatobus
426	60	13.0	541	2	Q5KNT3_CRYNE	Q5KNT3 cryptococcu	499	59	12.8	189	2	Q6X9L0_SULTS	Q6X9L0 sulfatobus
427	60	13.0	565	2	Q8VD01_MOUSE	Q8VD01 mus musculu	500	59	12.8	189	2	Q6X9L1_SULTS	Q6X9L1 sulfatobus
428	60	13.0	580	2	Q71195_CHICK	Q71195 gallus gall	501	59	12.8	189	2	Q6X9L7_SULTS	Q6X9L7 sulfatobus
429	60	13.0	605	2	Q7NHD8_GLOVI	Q7NHD8 gloobacter	502	59	12.8	199	2	Q6X9M0_SULTS	Q6X9M0 sulfatobus
430	60	13.0	611	2	Q8BYF6_MOUSE	Q8BYF6 m mus muscu	503	59	12.8	215	1	YCHE_ECOLI	P57343 escherichia
431	60	13.0	616	2	Q9Y1A2_TRYBB	Q9Y1A2 trypanosoma	504	59	12.8	215	2	Q8PHX1_ECOS6	Q8PHX1 escherichia
432	60	13.0	616	2	Q581Z5_9RRYP	Q581Z5 trypanosoma	505	59	12.8	215	2	Q83RNI_SHITL	Q83RNI shigella fl
433	60	13.0	756	2	Q55Z68_CRYNE	Q55Z68 cryptococcu	506	59	12.8	215	2	Q8XDA5_ECOS7	Q8XDA5 eschoc
434	60	13.0	793	2	Q94BY0_ARATH	Q94BY0 arabidopsis	507	59	12.8	284	2	Q594H3_9SPHN	Q594H3 agrobacteri
435	60	13.0	819	1	U66NL_MOUSE	Q80XC3 mus musculu	508	59	12.8	293	1	PUR7_BORBR	Q7wb15 bordetella
436	60	13.0	876	2	Q41TT5_AZOVI	Q41TT5 azotobacter	509	59	12.8	293	1	PUR7_BORBR	Q7wb15 bordetella
437	60	13.0	1056	2	Q4UVM2_XANCP	Q4UVM2 xanthomonas	510	59	12.8	293	1	PUR7_BORBR	Q7wb15 bordetella
438	60	13.0	1056	2	Q8PB75_XANCP	Q8PB75 xanthomonas	511	59	12.8	310	2	Q9A1T0_CAUCR	Q9A1T0 caulobacter
439	60	13.0	1157	2	Q6BHA0_DEBHA	Q6BHA0 debaryomyce	512	59	12.8	310	2	Q577P4_BRUBA	Q577P4 bruceella ab
440	60	13.0	1187	2	Q4S6R6_TETNG	Q4S6R6 tetradon n	513	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
441	60	13.0	5217	1	HTS1_COCCA	Q01886 cochllobolu	514	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
442	59.5	12.9	209	2	Q5KMO0_CRYNE	Q5KMO0 cryptococcu	515	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
443	59.5	12.9	214	2	Q7N4S9_PHOOL	Q7N4S9 photorhabdu	516	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
444	59.5	12.9	216	2	Q9GJG8_SALTR	Q9GJG8 salmo trutt	517	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
445	59.5	12.9	216	2	Q9GJG8_SALTR	Q9GJG8 salmo trutt	518	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
446	59.5	12.9	216	2	Q9GJH0_SALTR	Q9GJH0 salmo trutt	519	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
447	59.5	12.9	217	2	Q9GJH3_SALTR	Q9GJH3 salmo trutt	520	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
448	59.5	12.9	217	2	Q9GJH4_SALTR	Q9GJH4 salmo trutt	521	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
449	59.5	12.9	217	2	Q9GJH6_SALTR	Q9GJH6 salmo trutt	522	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
450	59.5	12.9	217	2	Q9GJH7_SALTR	Q9GJH7 salmo trutt	523	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
451	59.5	12.9	223	2	Q6PERS_MOUSE	Q6PERS mus musculu	524	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
452	59.5	12.9	228	2	Q4RUQ4_TETNG	Q4RUQ4 tetradon n	525	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
453	59.5	12.9	260	2	Q86A07_DICDI	Q86A07 dictyostei	526	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
454	59.5	12.9	267	2	Q8CG47_IACLA	Q8CG47 lactococcus	527	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
455	59.5	12.9	298	2	Q8GXR2_VIBCH	Q8GXR2 vibrio chol	528	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
456	59.5	12.9	341	2	Q880K3_PSESM	Q880K3 pseudomonas	529	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
457	59.5	12.9	342	2	Q8G5Z0_9SAUR	Q8G5Z0 pseudocallot	530	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
458	59.5	12.9	348	2	Q8XKMO_CLOPE	Q8XKMO clostetridium	531	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
459	59.5	12.9	356	2	Q9YMMO_NFVLDP	Q9YMMO lymantria d	532	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
460	59.5	12.9	384	2	Q72DS9_DESVLR	Q72DS9 desulfovibr	533	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
461	59.5	12.9	385	2	Q4SSP1_TETNG	Q4SSP1 tetradon n	534	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
462	59.5	12.9	396	2	Q9UJ33_CAERL	Q9UJ33 caenorhabdi	535	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
463	59.5	12.9	397	2	Q8XKS3_RALSO	Q8XKS3 ralfsonia s	536	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
464	59.5	12.9	426	2	Q6FJK9_CANGA	Q6FJK9 candida gla	537	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
465	59.5	12.9	431	2	Q7XTD3_ORYSA	Q7XTD3 oryza sativ	538	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
466	59.5	12.9	527	1	Q7VIO6_HEIHP	Q7VIO6 helicobacter	539	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
467	59.5	12.9	527	1	TH11_TRYBB	Q06221 trypanosoma	540	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
468	59.5	12.9	527	1	Q26765_9RRYP	Q26765 trypanosoma	541	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab
469	59.5	12.9	528	1	TH12_TRYBB	Q09037 trypanosoma	542	59	12.8	310	2	Q8FWG7_BRUBA	Q8FWG7 bruceella ab

543	59	12.8	655	1	KCN4A_RAT	P15385	rattus	novy	616	58.5	12.7	426	2	069513	MYCLE	069513	mycobacteri
544	59	12.8	660	1	KCN4A_BOVIN	005037	boe	taurus	617	58.5	12.7	463	2	09CB73	MYCLE	09CB73	mycobacteri
545	59	12.8	660	2	084MG5_ORYSA	084mg5	oryza	sativ	618	58.5	12.7	471	2	04S1G4	TETNG	04S1G4	tetrarodon n
546	59	12.8	661	2	09GLF1_BOVIN	09glf1	boe	taurus	619	58.5	12.7	482	2	097CF4	THEOG	097CF4	thermoplasm
547	59	12.8	662	2	090W36_CHOLI	090w36	columbia	liv	620	58.5	12.7	499	2	04NDZ1	9MTCC	04NDZ1	arthrobacte
548	59	12.8	662	2	09YXG8_GALLI	09YXG8	gallus	gall	621	58.5	12.7	509	2	08BNS5	9TRYP	08BNS5	trypanosoma
549	59	12.8	663	2	061VQ2_CAEBR	061VQ2	caenorhabd		622	58.5	12.7	516	2	084DM1	LISSE	084DM1	listeria se
550	59	12.8	697	2	084G57_XENLA	084G57	xenopus	lae	623	58.5	12.7	516	2	084DU3	LISSE	084DU3	listeria se
551	59	12.8	700	2	05R4E7_PONPY	05r4e7	pongo	pygma	624	58.5	12.7	557	2	08VZE2	ARATH	08VZE2	arthrobacte
552	59	12.8	771	2	080X33_MOUSE	080x33	mus	musculu	625	58.5	12.7	565	2	0833DE	COXBU	0833DE	coxiella bu
553	59	12.8	782	2	06LKY8_PHOFR	06lky8	photodact		626	58.5	12.7	587	2	091A29	ONGMY	091A29	oncorhynch
554	59	12.8	787	2	05SMW7_ORYSA	05smw7	oryza	sativ	627	58.5	12.7	633	2	04HWW9	GIBZE	04HWW9	gibberella
555	59	12.8	816	2	098SV4_ICTPU	098sv4	icetalurus	p	628	58.5	12.7	639	2	06VTM8	INPCD	06VTM8	invertebr
556	59	12.8	855	2	07NBTO_MYCGA	07nbto	mycoplasma		629	58.5	12.7	652	2	05CNT9	CRYHO	05CNT9	cryptospori
557	59	12.8	857	1	KCNB1_MOUSE	003117	mus	musculu	630	58.5	12.7	683	2	058QF6	WHEAT	058QF6	wheat
558	59	12.8	857	1	KCNB1_RAT	P15387	rattus	novy	631	58.5	12.7	716	2	058QF6	WHEAT	058QF6	wheat
559	59	12.8	857	1	08KOD1_MOUSE	08Kod1	mus	musculu	632	58.5	12.7	716	2	053UC8	WHEAT	053UC8	wheat
560	59	12.8	858	1	KCNB1_HUMAN	014721	homo	sapien	633	58.5	12.7	719	2	089ZNE	BACTN	089ZNE	bacteroides
561	59	12.8	858	1	KCNB1_PIG	018868	sus	scrofa	634	58.5	12.7	726	2	08HTN2	9MAGN	08HTN2	9mag
562	59	12.8	858	1	KCNB1_RABIT	09m159	oryctolagus		635	58.5	12.7	876	2	05FAJ3	NEIG1	05FAJ3	neisseria g
563	59	12.8	898	2	091592_XENLA	091592	xenopus	lae	636	58.5	12.7	878	2	05FAJ3	NEIG1	05FAJ3	neisseria g
564	59	12.8	907	1	KCNB2_RAT	063099	rattus	novy	637	58.5	12.7	1048	2	06EMD9	ECOLI	06EMD9	escherichia
565	59	12.8	911	1	KCNB2_HUMAN	092953	homo	sapien	638	58.5	12.7	1048	2	0605N9	KLEPN	0605N9	klebsiella
566	59	12.8	911	1	KCNB2_RABIT	095111	oryctolagus		639	58.5	12.7	1105	2	09C7H5	ARATH	09C7H5	arthrobacte
567	59	12.8	911	2	07Z7D0_HUMAN	07z7d0	homo	sapien	640	58.5	12.7	1105	2	05F3N7	CHICK	05F3N7	gallus gall
568	59	12.8	911	2	04ZHA6_BOVIN	04zha6	boe	taurus	641	58.5	12.7	1189	2	044415	9RHIZ	044415	agrobacteri
569	59	12.8	936	2	06GNA5_XENLA	06gna5	xenopus	lae	642	58.5	12.7	1346	2	053GR8	MAGCR	053GR8	magorthe
570	59	12.8	971	2	05AXB1_EMBNI	05axb1	aspergillus		643	58.5	12.7	1720	2	04FXS8	LEITMA	04FXS8	leishmania
571	59	12.8	1078	2	041S20_AZCVI	041s20	azotobacter		644	58.5	12.7	1817	2	07S2FE	XENLA	07S2FE	xenopus lae
572	59	12.8	1211	2	057WZ8_9TRYP	057wz8	trypanosoma		645	58.5	12.7	2473	2	09SLC7	9MAMM	09SLC7	tachyloesu
573	59	12.8	1463	2	04R3P5_USTMA	04r3p5	ustilago	ma	646	58.5	12.7	2710	2	0873G9	CABEL	0873G9	caenorhabd
574	58.5	12.7	133	2	08DA24_VIBVU	08da24	vibrio	vuln	647	58.5	12.7	2712	2	001808	CABEL	001808	caenorhabd
575	58.5	12.7	153	2	07MK55_VIBVY	07mk55	vibrio	vuln	648	58.5	12.7	5395	2	05VKR4	SACRC	05VKR4	saccharopol
576	58.5	12.7	169	2	06MLM7_BDEBA	06mlm7	bdellovibri		649	58.5	12.7	6193	2	08KSD0	STRCP	08KSD0	streptomyce
577	58.5	12.7	182	2	0916C9_PSEBA	0916c9	pseudomonas		650	58	12.6	96	2	083E08	COXBU	083E08	coxiella bu
578	58.5	12.7	196	2	07QBE9_ANOGA	07qbe9	anopheles	g	651	58	12.6	104	2	024949	FASHE	024949	faecicola he
579	58.5	12.7	196	1	CLPP_HEILH	07vnt9	helicobacte		652	58	12.6	114	1	YDGD	BACBU	YDGD	bacillus su
580	58.5	12.7	200	2	04TT87_CABEL	04tt87	caenorhabd		653	58	12.6	120	2	04J5Z8	AZCVI	04J5Z8	azotobacter
581	58.5	12.7	200	2	0852L5_ORYSA	0852l5	oryza	sativ	654	58	12.6	175	2	05WAS8	BACSK	05WAS8	bacillus cl
582	58.5	12.7	217	2	096XK6_SULTO	096xk6	sulfolobus		655	58	12.6	177	2	09BUM4	LISIN	09BUM4	listeria in
583	58.5	12.7	221	2	04SQX2_TETNG	04sqx2	tetrarodon	n	656	58	12.6	185	2	05PU65	SALPA	05PU65	salmonella
584	58.5	12.7	222	2	07N7R7_PHOLL	07n7r7	photorhabd		657	58	12.6	185	2	082152	SALTI	082152	salmonella
585	58.5	12.7	238	2	04SDB4_TETNG	04sdb4	tetrarodon	n	658	58	12.6	185	2	082K73	SALTY	082K73	salmonella
586	58.5	12.7	239	2	0661B5_BRABE	0661b5	brachyranio		659	58	12.6	196	2	09RYZ1	DEIRA	09RYZ1	deinococcus
587	58.5	12.7	260	1	NRPN_HUMAN	060259	homo	sapien	660	58	12.6	215	2	057NR2	SALCH	057NR2	salmonella
588	58.5	12.7	260	2	081W69_HUMAN	081w69	homo	sapien	661	58	12.6	215	2	05FC15	SALPA	05FC15	salmonella
589	58.5	12.7	260	2	088YT6_LACPL	088yt6	lactobacill		662	58	12.6	215	2	07CQF4	SALTY	07CQF4	salmonella
590	58.5	12.7	265	2	0603A7_MERCA	0603a7	methylcoccc		663	58	12.6	215	2	08XFE2	SALTI	08XFE2	salmonella
591	58.5	12.7	299	2	07W0P0_BORBE	07w0p0	borderella		664	58	12.6	232	2	05E000	VIBF1	05E000	vibrio fibc
592	58.5	12.7	299	2	07W3G6_BORBA	07w3g6	borderella		665	58	12.6	257	1	DPHB	METJA	DPHB	metanococc
593	58.5	12.7	299	2	07WET6_BORBR	07wet6	borderella		666	58	12.6	263	2	09FP64	ORYSA	09FP64	oryza sativ
594	58.5	12.7	299	2	07WUJ4_CHRVO	07wuj4	chromobacte		667	58	12.6	277	1	RAFR	PEDPE	RAFR	pedococcus
595	58.5	12.7	303	2	05XYK9_ARATH	05xyk9	arabidopsi		668	58	12.6	314	2	061K08	DROME	061K08	drosophila
596	58.5	12.7	321	1	TILS_BORPE	07v932	arabidopsi		669	58	12.6	325	2	09ELT9	JYVRU	09ELT9	rice grassy
597	58.5	12.7	328	2	06LEX6_PLAF7	06lex6	plasmodium		670	58	12.6	331	2	065F35	BACLD	065F35	bacillus li
598	58.5	12.7	336	2	082BR5_STRAM	082br5	streptomyce		671	58	12.6	333	2	08W7M6	HUMAN	08W7M6	homo sapien
599	58.5	12.7	340	2	08R782_THETN	08r782	thermoanaer		672	58	12.6	344	2	04V1K5	BACCC	04V1K5	ba
600	58.5	12.7	342	2	04NG06_9M1CC	04ng06	athrobacte		673	58	12.6	345	1	06AXV5	RAT	06AXV5	rattus novy
601	58.5	12.7	352	2	05BECR9_CANFA	05ecr9	canis	famil	674	58	12.6	349	2	07WGC8	VIBVY	07WGC8	vibrio vuln
602	58.5	12.7	352	2	05SKSV8_CANFA	05sksv8	arabidopsi		675	58	12.6	354	2	095HB3	ANAPL	095HB3	anae playtr
603	58.5	12.7	359	2	05LSUF2_CHLAB	05lsuf2	chlamydomo		676	58	12.6	368	2	023311	CABEL	023311	caenorhabd
604	58.5	12.7	366	2	0898R9_BRALJ	089tr9	bradyrhizob		677	58	12.6	376	2	0926X9	LISIN	0926X9	listeria in
605	58.5	12.7	372	1	FAD6E_ARATH	086x11	patarae	macu	678	58	12.6	383	2	081BN5	BACRC	081BN5	ba
606	58.5	12.7	383	1	FAD6E_ARATH	086x11	patarae	macu	679	58	12.6	383	2	081BN5	BACRC	081BN5	ba
607	58.5	12.7	383	2	081FZ8_ARATH	081fz8	arabidopsi		680	58	12.6	395	1	07PSF3	ANOGA	07PSF3	anog
608	58.5	12.7	384	2	08UAR7_AGRYS	08uar7	agrobacteri		681	58	12.6	398	2	SELI	MOUSE	SELI	mouse
609	58.5	12.7	385	2	06ZUL9_ORYSA	06z119	oryza	sativ	682	58	12.6	403	2	09KEH1	VIBCH	09KEH1	vibrio chol
610	58.5	12.7	392	2	07CS44_AGRYS	07cs44	agrobacteri		683	58	12.6	409	2	04MX56	BACCE	04MX56	ba
611	58.5	12.7	392	2	06C9T8_YARUT	06c9t8	yarrowia	li	684	58	12.6	411	2	07YQF7	OCHOPR	07YQF7	ochotona pr
612	58.5	12.7	400	1	EFTU_HERAV	08d247	hepsetosiph		685	58	12.6	440	2	04MSY3	BACCE	04MSY3	ba
613	58.5	12.7	409	1	08DBZ6_VIBVU	08dbz6	vibrio	vuln	686	58	12.6	440	2	06HKY9	BACCH	06HKY9	ba
614	58.5	12.7	411	2	09RU03_DEIRA	09ru03	deinococcus		687	58	12.6	440	2	081FL1	BACCR	081FL1	ba
615	58.5	12.7	425	1	YOSH_SCHPO	09p712	schizosacch		688	58	12.6	440	2	081FL1	BACCR	081FL1	ba

689	58	12.6	440	2	Q73A54_BACCI	Q73A64_bacillus ce	762	57.5	12.5	388	2	Q54466_STRMY	Q54466 streptomyc
690	58	12.6	440	2	Q63D66_BACCA	Q63D66 bacillus ce	763	57.5	12.5	401	2	Q87427_PODAN	Q87427 podopora a
691	58	12.6	440	2	Q81S04_BACAN	Q81S04 bacillus an	764	57.5	12.5	402	2	Q727Q2_HUMAN	Q727Q2 homo sapien
692	58	12.6	444	2	Q4SMG6_TETNG	Q4SMG6 tetradon n	765	57.5	12.5	426	2	Q57137_9BETA	Q57137 human herpe
693	58	12.6	448	2	Q84DP2_LISMO	Q84DP2 listeria mo	766	57.5	12.5	433	2	Q4H838_9DEIO	Q4H838 deinococcus
694	58	12.6	457	2	Q4KJF7_PSEPF	Q4KJF7 pseudomonas	767	57.5	12.5	441	2	Q60N14_CAEBR	Q60N14 ceenorhabdi
695	58	12.6	461	2	Q8ZRO7_SALTY	Q8ZRO7 salmonella	768	57.5	12.5	446	2	Q6H7Q3_ORYSA	Q6H7Q3 oryza sativ
696	58	12.6	462	2	Q8RYH5_DEIRA	Q8RYH5 deinococcus	769	57.5	12.5	448	2	Q6NBL7_RHOFA	Q6NBL7 rhodopseud
697	58	12.6	486	2	Q6DBW3_BRARE	Q6DBW3 brachydanio	770	57.5	12.5	453	2	Q7ZVN2_BRARE	Q7ZVN2 brachydanio
698	58	12.6	487	2	Q4T7M0_TETNG	Q4T7M0 tetradon n	771	57.5	12.5	461	2	Q5PM91_SALPA	Q5PM91 salmonella
699	58	12.6	511	2	Q74CB3_GEOSL	Q74CB3 geobacter s	772	57.5	12.5	461	2	Q8Z815_SALTI	Q8Z815 salmonella
700	58	12.6	541	2	Q9Y111_LOCOMI	Q9Y111 locusta mlg	773	57.5	12.5	461	2	Q916E1_PSEAR	Q916E1 pseudomonas
701	58	12.6	549	2	Q8GGR2_STRAZ	Q8GGR2 streptomyc	774	57.5	12.5	461	2	Q65QV2_MANSN	Q65QV2 manheimia
702	58	12.6	552	2	Q4J3Z2_AZOVI	Q4J3Z2 azotobacter	775	57.5	12.5	502	2	Q5V1D8_HALMA	Q5V1D8 haloarcula
703	58	12.6	553	2	Q942J6_ORYSA	Q942J6 oryza sativ	776	57.5	12.5	507	2	Q5PPFS_RAT	Q5PPFS rattus norv
704	58	12.6	619	2	Q7UVX4_RHOBA	Q7UVX4 rhodopirell	777	57.5	12.5	517	2	Q8EVA5_MYCPB	Q8EVA5 mycoplasma
705	58	12.6	624	2	Q86146_CAMJE	Q86146 campylobact	778	57.5	12.5	523	2	Q916Z6_PSEAR	Q916Z6 pseudomonas
706	58	12.6	674	2	Q8BHZ1_XANAC	Q8BHZ1 xanthomonas	779	57.5	12.5	528	1	KCNJ13_MOUSE	P16390 mus musculu
707	58	12.6	675	2	Q5H2Z6_XANOR	Q5H2Z6 xanthomonas	780	57.5	12.5	531	2	Q8BRG1_OCEBH	Q8BRG1 oceanobacil
708	58	12.6	676	2	Q8XQ93_RALSO	Q8XQ93 ralstonia s	781	57.5	12.5	541	2	Q4SEY1_TETNG	Q4SEY1 tetradon n
709	58	12.6	681	1	GAZL1_HUMAN	Q93501 homo sapien	782	57.5	12.5	574	2	Q8XQ27_RALSO	Q8XQ27 ralstonia s
710	58	12.6	682	1	Q4HUI4_GIBZE	Q4HUI4 glibberella	783	57.5	12.5	581	2	Q6BK68_DEBHA	Q6BK68 debaryomyce
711	58	12.6	695	2	Q4HLX6_CAMLA	Q4HLX6 campylobact	784	57.5	12.5	594	2	Q98PX5_MYCPV	Q98PX5 mycoplasma
712	58	12.6	743	2	Q6FUV9_CANGA	Q6FUV9 candida gla	785	57.5	12.5	603	2	Q4P4K6_USTWA	Q4P4K6 ustula ma
713	58	12.6	758	2	Q9VQW0_DROME	Q9VQW0 drosophila	786	57.5	12.5	636	2	Q86486_PPARA	Q86486 piperast
714	58	12.6	767	2	Q51CIV0_ENTHI	Q51CIV0 entamoeba h	787	57.5	12.5	636	2	Q8K244_MOUSE	Q8K244 mus musculu
715	58	12.6	778	2	Q60ZP1_CAEBR	Q60ZP1 caenorhabdi	788	57.5	12.5	662	1	HEPA_HHV62	P82451 human herpe
716	58	12.6	876	2	Q91593_XENLA	Q91593 xenopus lae	789	57.5	12.5	662	2	Q9WT01_9BETA	Q9WT01 human herpe
717	58	12.6	978	2	Q5BDP3_EMENT	Q5BDP3 aspergillus	790	57.5	12.5	668	2	Q4UKH5_XANCP	Q4UKH5 xanthomonas
718	58	12.6	1006	2	Q4N149_9MICC	Q4N149 aspergillus	791	57.5	12.5	668	2	Q8P6N7_XANCP	Q8P6N7 xanthomonas
719	58	12.6	1018	2	Q6ALX0_DESPS	Q6ALX0 desulfotale	792	57.5	12.5	670	2	Q9BNA0_9MANC	Q9BNA0 manihoti
720	58	12.6	1051	2	Q5S9V4_EMENT	Q5S9V4 aspergillus	793	57.5	12.5	671	2	Q5AKV5_CANAL	Q5AKV5 candida alb
721	58	12.6	1056	2	Q7S8Q2_NEUCR	Q7S8Q2 neurospora	794	57.5	12.5	692	2	Q9BAR1_9MAGN	Q9BAR1 buxus glome
722	58	12.6	1056	2	Q8BUN1_XANAC	Q8BUN1 xanthomonas	795	57.5	12.5	745	1	PURL_HELHP	Q159G2 enthi
723	58	12.6	1109	2	Q7JRS2_DROME	Q7JRS2 drosophila	796	57.5	12.5	750	2	Q519G2_ENTHI	Q519G2 ceenorhabdi
724	58	12.6	1135	2	Q9V7B8_DROME	Q9V7B8 drosophila	797	57.5	12.5	771	2	Q617U6_CAEBR	Q617U6 caenorhabdi
725	58	12.6	1149	2	Q7KUP4_DROME	Q7KUP4 drosophila	798	57.5	12.5	772	2	Q75JF4_DICDI	Q75JF4 dictyosteli
726	58	12.6	1821	2	Q7PQL1_ANOGA	Q7PQL1 anopheles g	799	57.5	12.5	794	2	Q6P40_XENLA	Q6P40 xenopus lae
727	58	12.6	1905	2	Q9XTE6_PLABE	Q9XTE6 plasmodium	800	57.5	12.5	822	2	Q81ON2_DROME	Q81ON2 drosophila
728	58	12.6	2576	2	Q4UFV5_BRARE	Q4UFV5 brachydanio	801	57.5	12.5	857	1	OPGH_PSEPK	Q68D40 pseudomonas
729	58	12.6	4836	2	Q4UZRI_MOUSE	Q4UZRI mus musculu	802	57.5	12.5	865	2	Q61J98_CAEBR	Q61J98 ceenorhabdi
730	58	12.6	4836	2	Q88473_MOUSE	Q88473 mus musculu	803	57.5	12.5	882	2	Q8MOK2_DROME	Q8MOK2 drosophila
731	57.5	12.5	71	1	VITB2_XENLA	P19011 xenopus lae	804	57.5	12.5	907	2	Q8VY10_ARATH	Q8VY10 arabidopsis
732	57.5	12.5	84	2	Q8TFE5_DROPS	Q8TFE5 drosophila	805	57.5	12.5	1012	2	Q8XDM5_RALSO	Q8XDM5 ralstonia s
733	57.5	12.5	128	2	Q9NG96_MAMBR	Q9NG96 mamestra br	806	57.5	12.5	1071	2	Q993F2_9GAMA	Q993F2 callitriche
734	57.5	12.5	129	2	Q4K8V9_PSEFS	Q4K8V9 pseudomonas	807	57.5	12.5	1625	2	Q6MVD4_NEUCR	Q6MVD4 neurospora
735	57.5	12.5	139	2	Q8Z6V7_SALTI	Q8Z6V7 salmonella	808	57.5	12.5	1681	2	Q4SVT8_TETNG	Q4SVT8 tetradon n
736	57.5	12.5	144	2	Q5YXC3_NOCFA	Q5YXC3 nocardia fa	809	57.5	12.5	1696	2	Q4NOK7_THERP	Q4NOK7 theileria p
737	57.5	12.5	144	2	Q9BRP0_RAT	Q9BRP0 rattus norv	810	57.5	12.5	1751	2	Q57V95_STRYP	Q57V95 streptococ
738	57.5	12.5	146	2	Q5LSS1_SILPO	Q5LSS1 silicibacte	811	57.5	12.5	1902	1	CHD7_HUMAN	Q60ZNS CAEBR
739	57.5	12.5	153	2	Q8K071_MOUSE	Q8K071 mus musculu	812	57.5	12.5	2235	1	Q60ZNS CAEBR	Q60ZNS ceenorhabdi
740	57.5	12.5	173	2	Q8SCX0_9TELE	Q8SCX0 salangichth	813	57.5	12.5	2322	2	Q4N127_THERP	Q4N127 theileria p
741	57.5	12.5	184	2	Q5U4U5_XENLA	Q5U4U5 xenopus lae	814	57.5	12.5	3300	2	Q4FTT0_9GAMW	Q4FTT0 9GAMW
742	57.5	12.5	194	2	Q5BIN1_BOVIN	Q5BIN1 bos taurus	815	57	12.4	105	2	Q8LGH9_ARATH	Q8LGH9 arabidopsis
743	57.5	12.5	224	1	CLPPI1_SYNPX	Q7NA36 synnechococ	816	57	12.4	148	2	Q9ZV24_ARATH	Q9ZV24 arabidopsis
744	57.5	12.5	242	2	Q83TJ3_SALTI	Q83TJ3 salmonella	817	57	12.4	148	2	Q9ZV24_ARATH	Q9ZV24 arabidopsis
745	57.5	12.5	255	2	Q7XQ06_ORYSA	Q7XQ06 oryza sativ	818	57	12.4	152	2	Q8ES95_STRJ3	Q8ES95 streptococ
746	57.5	12.5	292	2	Q6FUC0_CANGA	Q6FUC0 candida gla	819	57	12.4	158	2	Q6FSW5_CANGA	Q6FSW5 candida gla
747	57.5	12.5	303	2	Q46720_ECOLI	Q46720 escherichia	820	57	12.4	166	2	Q61JUI_DROME	Q61JUI drosophila
748	57.5	12.5	313	2	Q7NMF7_CHRVO	Q7NMF7 chromobacte	821	57	12.4	171	2	Q5COK4_SCHJA	Q5COK4 schistosoma
749	57.5	12.5	323	2	Q93H09_STRCO	Q93H09 streptomyc	822	57	12.4	177	2	Q5IKR5_SILPO	Q5IKR5 silicibacte
750	57.5	12.5	324	2	Q9S248_STRCO	Q9S248 streptomyc	823	57	12.4	184	2	Q8LE27_ARATH	Q8LE27 arabidopsis
751	57.5	12.5	337	2	Q817B2_FASHE	Q817B2 fasciola he	824	57	12.4	184	2	Q4TMQ7_9SPHN	Q4TMQ7 9SPHN
752	57.5	12.5	342	1	IS1A_SYNP2	P13157 synnechococ	825	57	12.4	185	1	ADML_RAT	ADML_RAT
753	57.5	12.5	353	2	Q9LR55_ARATH	Q9LR55 arabidopsis	826	57	12.4	190	1	PYRE_THERTN	Q83TM7_LISMO
754	57.5	12.5	355	2	Q4JFC3_MOUSE	Q4JFC3 mus musculu	827	57	12.4	228	2	Q8EG49_SHEON	Q8EG49 sheenella
755	57.5	12.5	356	2	Q9Y941_AERPE	Q9Y941 aeropyrum p	828	57	12.4	230	2	Q658A8_ORYSA	Q658A8 oryza sativ
756	57.5	12.5	363	2	Q6D013_ERWCT	Q6D013 erwinia car	829	57	12.4	241	2	Q61095_TRYCR	Q61095 trypanosoma
757	57.5	12.5	371	2	Q53GK2_HUMAN	Q53GK2 homo sapien	830	57	12.4	254	2	UDP_TREBA	Q70FH9 uncultured
758	57.5	12.5	371	2	Q9J8C7_9NUCL	Q9J8C7 podopocera	831	57	12.4	258	1	Q61095_TRYCR	Q61095 trypanosoma
759	57.5	12.5	379	1	Q8E6_NFYOP	Q8E6_NFYOP	832	57	12.4	268	2	Q70FH9_9CYAN	Q70FH9 uncultured
760	57.5	12.5	379	1	MCP_CAVPO	P81053 cavia porce	833	57	12.4	269	2	Q8XW00_ANASP	Q8XW00 anaplasma
761	57.5	12.5	383	2	Q8A186_BACTN	Q8A186 bacteroides	834	57	12.4	276	2	Q68E53_XENLA	Q68E53 xenopus lae

835	57	12.4	283	2	Q4V7U2_XENLA	Q4V7U2 xenopus lae	908	57	12.4	811	2	Q4EX22_LEIMA	Q4EX22 telestania
836	57	12.4	291	2	Q5WX66_LEGPL	Q5WX66 legioneila	909	57	12.4	858	2	Q6EP87_MOUSE	Q6EP87 mus musculus
837	57	12.4	292	2	Q6UY47_HUMAN	Q6UY47 homo sapien	910	57	12.4	880	2	Q6K107_MYCWO	Q6K107 mycoplasma
838	57	12.4	301	2	Q8BYJ2_MOUSE	Q8BYJ2 mus musculus	911	57	12.4	892	2	Q5LDM6_SILPO	Q5LDM6 silicibacte
839	57	12.4	302	2	Q768S4_MOUSE	Q768S4 mus musculus	912	57	12.4	953	1	FNBRJ3_MOUSE	FNBRJ3 mus musculus
840	57	12.4	315	2	Q9UNE2_HUMAN	Q9UNE2 homo sapien	913	57	12.4	1056	2	Q5GZ12_XANOR	Q5GZ12 xanthomonas
841	57	12.4	325	2	Q9QN99_YAVIU	Q9QN99 rice grassy	914	57	12.4	1137	2	Q8Z810_STRAW	Q8Z810 streptomyce
842	57	12.4	332	2	Q52M67_PAVLU	Q52M67 pavlova lut	915	57	12.4	1151	2	Q754S3_ASHGO	Q754S3 ashbya gosb
843	57	12.4	334	2	Q52M83_BANAT	Q52M83 bangia atro	916	57	12.4	1294	2	Q50HM7_STRSH	Q50HM7 streptomyce
844	57	12.4	342	1	ISIA_STNP7	ISIA_STNP7	917	57	12.4	1491	2	Q5GFT1_HAEIN	Q5GFT1 haemophilus
845	57	12.4	342	2	Q5N675_STNP6	Q5N675 synechococ	918	57	12.4	1574	2	Q7Y5J5_9CAUD	Q7Y5J5 xanthomonas
846	57	12.4	343	2	Q5LMB6_SILPO	Q5LMB6 silicibacte	919	57	12.4	1639	2	Q54J43_DICDI	Q54J43 dictyostell
847	57	12.4	351	2	Q97774_FELCA	Q97774 felis silve	920	57	12.4	1875	2	Q5X8U3_LEGPA	Q5X8U3 legioneila
848	57	12.4	352	2	Q867D6_FELCA	Q867D6 felis silve	921	57	12.4	2660	2	Q7OL19_ANOGA	Q7OL19 anopheles
849	57	12.4	353	2	Q9LR37_ARATH	Q9LR37 arabidopsis	922	57	12.4	3196	2	Q6ALOS_DSPPS	Q6ALOS denulifolae
850	57	12.4	355	2	Q5QNA9_ORYSA	Q5QNA9 oryza sativ	923	57	12.4	3338	2	Q82PH6_STRAW	Q82PH6 streptomyce
851	57	12.4	355	2	Q8WBK1_9AVES	Q8WBK1 saurothera	924	56.5	12.3	104	2	Q6J2H4_PSEYM	Q6J2H4 pseudomonas
852	57	12.4	360	2	Q80638_ARATH	Q80638 arabidopsis	925	56.5	12.3	107	2	Q67MA1_SYWTH	Q67MA1 synechobacte
853	57	12.4	374	2	Q9SVF3_ARATH	Q9SVF3 arabidopsis	926	56.5	12.3	110	2	Q6V932_9ILLI	Q6V932 xerophyta h
854	57	12.4	374	2	Q672B8_ARATH	Q672B8 arabidopsis	927	56.5	12.3	114	1	HKD3_RAT	HKD3 rat
855	57	12.4	374	2	Q5NWX2_AZOSE	Q5NWX2 azocarcus ap	928	56.5	12.3	120	2	Q6JIA6_HUMAN	Q6JIA6 homo sapien
856	57	12.4	376	2	Q6FVJ8_CANGA	Q6FVJ8 candida gla	929	56.5	12.3	120	2	Q4MP5_MOUSE	Q4MP5 bacillus ce
857	57	12.4	383	2	Q6HGU3_BACHK	Q6HGU3 bacillus th	930	56.5	12.3	120	2	Q6HMB7_BACHK	Q6HMB7 bacillus th
858	57	12.4	383	2	Q81NM9_BACAN	Q81NM9 bacillus an	931	56.5	12.3	120	2	Q63EV5_BAC2Z	Q63EV5 bacillus ce
859	57	12.4	384	2	Q6SX10_ORYSA	Q6SX10 oryza sativ	932	56.5	12.3	143	2	Q81U42_BACAN	Q81U42 bacillus an
860	57	12.4	385	2	Q9S2G0_ARATH	Q9S2G0 arabidopsis	933	56.5	12.3	143	2	Q8PLM5_XANAC	Q8PLM5 xanthomonas
861	57	12.4	386	2	Q5NFP0_FRATT	Q5NFP0 fransciella	934	56.5	12.3	145	2	Q7SLTO_HUMAN	Q7SLTO homo sapien
862	57	12.4	387	2	Q5B694_EMENTI	Q5B694 aspergillus	935	56.5	12.3	145	2	Q869G4_LYMST	Q869G4 lymnaea ste
863	57	12.4	387	2	Q6AQC6_DSPPS	Q6AQC6 desulifolae	936	56.5	12.3	148	2	Q9D2U7_MOUSE	Q9D2U7 mus musculus
864	57	12.4	399	2	Q5JU03_SHIFL	Q5JU03 shigella fl	937	56.5	12.3	148	2	Q9JLS0_MOUSE	Q9JLS0 mus musculus
865	57	12.4	409	2	Q639H1_BACC2	Q639H1 bacillus ce	938	56.5	12.3	170	2	Q9W2N2_DROME	Q9W2N2 drosophila
866	57	12.4	425	2	Q4TR85_9SBPN	Q4TR85 erythrobact	939	56.5	12.3	186	2	Q6N191_RHOPA	Q6N191 rhodospendo
867	57	12.4	440	2	Q9LNU8_ARATH	Q9LNU8 arabidopsis	940	56.5	12.3	187	2	Q52296_SHIFL	Q52296 shigella fl
868	57	12.4	440	2	Q8BJGO_MOUSE	Q8BJGO mus musculi	941	56.5	12.3	187	2	Q7BEL2_SHIFL	Q7BEL2 shigella fl
869	57	12.4	456	2	Q97N14_CLOAB	Q97N14 clostridium	942	56.5	12.3	188	2	Q5FRN2_GLUOX	Q5FRN2 glucinobact
870	57	12.4	457	1	PROY_ECOLI	PROY_ECOLI	943	56.5	12.3	190	2	Q9JKW1_RAT	Q9JKW1 rattus norv
871	57	12.4	457	1	Q83SG9_SHIFL	Q83SG9 shigella fl	944	56.5	12.3	191	2	Q57JF1_SALCH	Q57JF1 salmonella
872	57	12.4	461	1	DCUC_ECOLI	DCUC_ECOLI	945	56.5	12.3	191	2	Q5PLD9_SALPA	Q5PLD9 saltpa
873	57	12.4	461	2	Q57RU8_SALCH	Q57RU8 salmonella	946	56.5	12.3	191	2	Q7CPPO_SALTY	Q7CPPO salmoneila
874	57	12.4	461	2	Q8FJZ8_ECOL6	Q8FJZ8 escherichia	947	56.5	12.3	191	2	Q8XGY6_SALTI	Q8XGY6 salmonella
875	57	12.4	461	2	Q63M54_BURPS	Q63M54 burkholderi	948	56.5	12.3	194	1	TTM22_MOUSE	TTM22 mus musculus
876	57	12.4	468	2	Q7OD04_ANOGA	Q7OD04 anopheles g	949	56.5	12.3	194	1	Q5SSLI_MOUSE	Q5SSLI mus musculus
877	57	12.4	471	2	Q5JNB5_ORYSA	Q5JNB5 oryza sativ	950	56.5	12.3	195	2	Q9JKW2_MOUSE	Q9JKW2 mus musculus
878	57	12.4	477	2	Q84DP6_LISMO	Q84DP6 listeria mo	951	56.5	12.3	195	2	Q81N78_DROME	Q81N78 drosophila
879	57	12.4	477	2	Q84DP7_LISMO	Q84DP7 listeria mo	952	56.5	12.3	197	2	Q8UOL2_PYRPU	Q8UOL2 pyrococcus
880	57	12.4	477	2	Q84DP8_LISMO	Q84DP8 listeria mo	953	56.5	12.3	197	2	Q73KTE_TREDE	Q73KTE treponema d
881	57	12.4	477	2	Q84DP9_LISMO	Q84DP9 listeria mo	954	56.5	12.3	211	2	Q6EST5_FUGRU	Q6EST5 figu rubrip
882	57	12.4	477	2	Q84DQ0_LISMO	Q84DQ0 listeria mo	955	56.5	12.3	213	2	Q8NS64_CORGL	Q8NS64 corynebacte
883	57	12.4	477	2	Q83TQ3_LISMO	Q83TQ3 listeria mo	956	56.5	12.3	214	2	Q4V6C7_DROME	Q4V6C7 drosophila
884	57	12.4	477	2	Q722W8_LISMF	Q722W8 listeria mo	957	56.5	12.3	228	2	Q84WK4_ARATH	Q84WK4 arabidopsis
885	57	12.4	478	2	Q84DN9_LISMO	Q84DN9 listeria mo	958	56.5	12.3	231	2	Q7UJW2_RHOBA	Q7UJW2 rhodopirell
886	57	12.4	478	2	Q84DS7_LISMO	Q84DS7 listeria mo	959	56.5	12.3	233	1	LEPX_MYCHO	LEPX mycobacteri
887	57	12.4	487	1	P5BC_FORPU	P51356 porphyra pu	960	56.5	12.3	233	1	LEPX_MYCTU	P63307 mycobacteri
888	57	12.4	487	1	P5BC_FORPU	P51356 porphyra pu	961	56.5	12.3	234	1	Q92LX9_RHIME	P63306 mycobacteri
889	57	12.4	487	2	Q93ZU2_ARATH	Q93ZU2 arabidopsis	962	56.5	12.3	244	2	Q8KZG6_MOUSE	Q8KZG6 mycobacteri
890	57	12.4	493	2	Q7NCL3_MYCGA	Q7NCL3 mycoplasma	963	56.5	12.3	258	2	Q8HP14_HALSA	Q8HP14 halobacteri
891	57	12.4	494	1	ILVC_PHOPR	Q61VZ5 photobacter	964	56.5	12.3	274	2	Q4SEPT_TETNG	Q4SEPT terradon n
892	57	12.4	517	2	Q88GM6_PSEPK	Q88GM6 pseudomonas	965	56.5	12.3	276	2	Q937L7_9CYAN	Q937L7 uncultured
893	57	12.4	531	2	Q6OVX5_CABER	Q6OVX5 caenorhabdi	966	56.5	12.3	276	2	Q937L8_9CYAN	Q937L8 uncultured
894	57	12.4	534	2	Q4WG10_ASPEFU	Q4WG10 aspergillus	967	56.5	12.3	288	2	Q826V5_STRAW	Q826V5 streptomyce
895	57	12.4	535	2	Q4KIR3_PSEFP	Q4KIR3 pseudomonas	968	56.5	12.3	299	2	Q4SGT7_TETNG	Q4SGT7 terradon n
896	57	12.4	576	2	Q8BYE8_MOUSE	Q8BYE8 mus musculi	969	56.5	12.3	304	2	Q4H8A0_9DEIO	Q4H8A0 deniococcus
897	57	12.4	606	2	Q88AM8_PSEBSM	Q88AM8 pseudomonas	970	56.5	12.3	305	2	Q5ZTIU9_CHICK	Q5ZTIU9 gallus gall
898	57	12.4	610	2	Q72ZM9_HUMAN	Q72ZM9 homo sapien	971	56.5	12.3	335	2	Q8G6M8_BIFLO	Q8G6M8 bifidobacte
899	57	12.4	610	2	Q8N695_HUMAN	Q8N695 homo sapien	972	56.5	12.3	337	1	TH23_TRYBB	TH23 trypanosoma
900	57	12.4	629	2	Q413Y7_GIBZE	Q413Y7 gibberella	973	56.5	12.3	337	1	Q9GKES_RABIT	Q9GKES coryctolagus
901	57	12.4	633	2	Q746H7_THET2	Q746H7 theinus the	974	56.5	12.3	350	2	Q7UXC7_RHOBA	Q7UXC7 rhodopirell
902	57	12.4	641	2	Q8MMD4_RABIT	Q8MMD4 coryctolagus	975	56.5	12.3	354	2	Q6ODT9_ORYSA	Q6ODT9 oryza sativ
903	57	12.4	689	2	Q6A4I8_BURFI	Q6A4I8 butyrivibri	976	56.5	12.3	358	2	Q4UKP7_RICPE	Q4UKP7 rickettsia
904	57	12.4	699	2	Q7NII1_GLOVI	Q7NII1 gloeobacter	977	56.5	12.3	364	2	Q4P219_USTMA	Q4P219 usciilago ma
905	57	12.4	705	2	Q4T7V1_TETNG	Q4T7V1 tetradon n	978	56.5	12.3	368	2	Q5YVAB_NOCFA	Q5YVAB nocardia fa
906	57	12.4	792	2	Q4RXCB_TETNG	Q4RXCB tetradon n	979	56.5	12.3	372	2	Q5QNB2_ORYSA	Q5QNB2 oryza sativ
907	57	12.4	802	2	Q7UMP8_RHOBA	Q7UMP8 rhodopirell	980	56.5	12.3	374	2	Q517H1_NPVAP	Q517H1 antheraea p

981	56.5	12.3	387	2	Q88L10_PRRPK	Q88I10_pseudomonas	1054	56.5	12.3	758	2	Q811T2_RAT	Q811t2_rattus norv
982	56.5	12.3	391	2	Q6MLC9_BDEBA	Q6mLc9_bdeliovibrio	1055	56.5	12.3	759	2	Q8HXV1_RABIT	Q8hXv1_oryctolagus
983	56.5	12.3	393	2	Q81JG4_BACAN	Q81Jg4_bacillus an	1056	56.5	12.3	769	2	Q811T3_RAT	Q811t3_rattus norv
984	56.5	12.3	394	2	Q7QA4_ANOGA	Q7QA4_anopheles g	1057	56.5	12.3	783	2	Q5NXT1_AZOSE	Q5nXt1_aeococcus sp
985	56.5	12.3	398	2	Q8LRB6_ORYSA	Q8lRb6_oryza sativ	1058	56.5	12.3	852	1	YKML_YEAST	P233t1_saccharomyc
986	56.5	12.3	403	2	Q7W0P4_BOORPE	Q7w0P4_bordetella	1059	56.5	12.3	856	1	Q6G4Z9_BARRH	Q6G4z9_bartonella
987	56.5	12.3	403	2	Q7W3G0_BOORPE	Q7w3G0_bordetella	1060	56.5	12.3	889	1	KCNK3_RAT	Q01956_rattus norv
988	56.5	12.3	403	2	Q7WET0_BOORPE	Q7wEt0_bordetella	1061	56.5	12.3	894	2	Q5CNG7_CRYHO	Q5cNg7_cryptospori
989	56.5	12.3	407	2	Q4J3Y8_AZOVI	Q4J3y8_azotobacter	1062	56.5	12.3	933	2	Q83GL1_TROWM	Q83gl1_tropheryma
990	56.5	12.3	408	2	Q6LM16_PHOFR	Q6lM16_photobacter	1063	56.5	12.3	939	2	Q83HL6_TROWM	Q83hl6_tropheryma
991	56.5	12.3	409	2	Q6LM16_PHOFR	Q6lM16_photobacter	1064	56.5	12.3	1000	2	Q5U6Z5_HUMAN	Q5u6Z5_homo sapien
992	56.5	12.3	411	2	Q7P149_CHRYVO	Q7p149_chromobacter	1065	56.5	12.3	1009	2	Q5QZ08_IDILLO	Q5qZ08_idiomarina
993	56.5	12.3	414	2	Q4SS40_TENG	Q4sS40_tetradodon n	1066	56.5	12.3	1030	1	SEME6_HUMAN	Q42e08_homo sapien
994	56.5	12.3	418	2	Q96U9_HUMAN	Q9eJ99_homo sapien	1067	56.5	12.3	1058	2	Q5P5T6_AZOSE	Q5p5T6_azotobacter
995	56.5	12.3	419	1	CARP_CRYPA	P11838_cryptonecetr	1068	56.5	12.3	1127	2	Q4Y0S5_PLABE	Q4y0S5_plasmodium
996	56.5	12.3	422	2	Q5PB80_HANAM	Q5pb80_anaplasma m	1069	56.5	12.3	1241	2	Q60RT2_CAEBR	Q60rT2_caenorhabdi
997	56.5	12.3	428	2	Q5PH29_HUMAN	Q5ph29_homo sapien	1070	56.5	12.3	1250	2	Q4PIV2_ISTMA	Q4pIv2_ustiliago ma
998	56.5	12.3	442	2	Q5OX17_IDILLO	Q5ox17_idiomarina	1071	56.5	12.3	1643	2	Q5ZCN4_ORYSA	Q5zCn4_oryza sativ
999	56.5	12.3	464	1	NORM_STNPE	Q5mzd9_eynechococc	1072	56.5	12.3	1739	2	Q4SKM5_TETNG	Q4sKm5_tetradodon n
1000	56.5	12.3	468	1	Q6JPM6_BURPS	Q6JpM6_burkholderi	1073	56.5	12.3	1778	2	Q414N8_GIBZE	Q414n8_gibberella
1001	56.5	12.3	468	2	Q6ZG62_BURMA	Q6Zg62_burkholderi	1074	56.5	12.3	1838	2	Q6BCJ9_TETTH	Q6bcJ9_tetrahymena
1002	56.5	12.3	471	2	Q49635_ARATH	Q49635_arabidopsis	1075	56.5	12.3	1844	2	Q5BDM2_EMENT	Q5bDm2_aspergillus
1003	56.5	12.3	474	2	Q5SMW4_CRYNE	Q5sW49_cryptococcu	1076	56.5	12.3	2113	2	Q4RMA1_TETNG	Q4rMa1_tetradodon n
1004	56.5	12.3	484	2	Q8SDM4_9CAUD	Q8sdM4_staphylococ	1077	56.5	12.3	2217	2	Q6FMT7_CANGA	Q6fM7_candida gla
1005	56.5	12.3	484	2	Q4ZCK1_9VIRU	Q4zCk1_bacteriopho	1078	56.5	12.3	2876	2	Q4QB73_LEIMA	Q4qb73_leishmania
1006	56.5	12.3	484	2	Q6GG84_STPAC	Q6gg84_staphylococ	1079	56.5	12.3	4464	2	Q7RLJ6_PLAYO	Q7rlJ6_plasmodium
1007	56.5	12.3	484	2	Q5H1X6_STPAC	Q5h1X6_staphylococ	1080	56.5	12.3	75	2	Q8E590_STRJ3	Q8e590_streptococc
1008	56.5	12.3	485	2	Q7CZRT_AGRF5	Q7cZrT_agrobacteri	1081	56	12.1	79	1	IVBK1_DENPO	P00981_dendotoxap
1009	56.5	12.3	485	2	Q90YX3_XENLA	Q90Yx3_xenopus lae	1082	56	12.1	100	2	Q6N984_RHOPA	Q6n984_rhodospseudo
1010	56.5	12.3	491	2	Q4RCUS_USTMA	Q4rCus_ustiliago ma	1083	56	12.1	103	1	NIRC_PANDE	Q51702_paracoccus
1011	56.5	12.3	494	2	Q86S12_9PIPT	Q86s12_drosophila	1084	56	12.1	103	2	Q8KZM1_MOUSE	Q8kZm1_mus musculu
1012	56.5	12.3	500	2	Q97KA2_CIOAB	Q97Ka2_clostridium	1085	56	12.1	126	2	Q57J16_9BACT	Q57J16_uncultured
1013	56.5	12.3	510	1	Q9RF10_MYXXX	Q9rF10_myxococcus	1086	56	12.1	126	2	Q6J5M4_ECOLI	Q6J5m4_eshcherichia
1014	56.5	12.3	511	1	ZGPAT_MOUSE	Q8vdm1_mus musculu	1087	56	12.1	146	2	Q4NYQ0_9DELT	Q4nyQ0_aeromonxyob
1015	56.5	12.3	521	2	Q7RYH0_NEUCR	Q7ryH0_neurospora	1088	56	12.1	160	2	Q61N07_CAEBR	Q61n07_caenorhabdi
1016	56.5	12.3	523	2	Q567M8_BRARE	Q567m8_brachydantio	1089	56	12.1	177	2	Q6Z5Y9_GIALA	Q6z5Y9_giardia lam
1017	56.5	12.3	529	1	THA2_TRYBB	Q06222_trypanosoma	1090	56	12.1	177	2	Q7R002_GIALA	Q7r002_giardia lam
1018	56.5	12.3	531	2	Q4UX17_CORUK	Q4UX17_corynebacte	1091	56	12.1	196	1	Y2B6_MYCBE	P75528_mycoplasma
1019	56.5	12.3	567	2	Q4K108_PSEFS	Q4K108_pseudomonas	1092	56	12.1	197	2	Q5FJH6_GLUOX	Q5fJh6_glycocabact
1020	56.5	12.3	570	2	Q4WD85_ASPFU	Q4wD85_aspergillus	1093	56	12.1	212	2	Q87MV9_VIBPA	Q87mV9_vibrio para
1021	56.5	12.3	572	2	Q8S0S0_9INSE	Q8s0S0_ritcholepid	1094	56	12.1	218	2	Q9D692_MOUSE	Q9d692_mus musculu
1022	56.5	12.3	595	1	S13A1_HUMAN	Q8pZw2_homo sapien	1095	56	12.1	220	2	Q5LBE4_BACRN	Q5lEb4_bacteroides
1023	56.5	12.3	608	2	Q9BAR2_9MAGN	Q9bAr2_nocodbuxus n	1096	56	12.1	222	2	Q9KVF5_VIBCH	Q9kVf5_vibrio chol
1024	56.5	12.3	614	2	Q31615_BACSU	Q31615_bacillus su	1097	56	12.1	228	2	Q5J432_SALCH	Q5J432_salmonella
1025	56.5	12.3	624	2	Q69Z90_MOUSE	Q69Z90_mus musculu	1098	56	12.1	230	2	Q5QLP9_ORYSA	Q5qLp9_oryza sativ
1026	56.5	12.3	648	2	Q5FJH5_GLUOX	Q5fJh5_glycocabact	1099	56	12.1	242	2	Q6ME49_PARUM	Q6me49_parachlamyd
1027	56.5	12.3	670	2	Q3Z212_BACSU	Q3Z212_bacillus su	1100	56	12.1	249	2	Q5VTN6_BRARE	Q5vTn6_brachydantio
1028	56.5	12.3	681	2	Q9BAO3_9MAGN	Q9baQ3_nocodbuxus a	1101	56	12.1	254	2	Q91207_ONCMY	Q91207_oncorhynch
1029	56.5	12.3	683	2	Q5CVZ7_CRYPV	Q5cVZ7_cryptospori	1102	56	12.1	261	2	Q8UAP2_AGRF5	Q8uAp2_agrobacteri
1030	56.5	12.3	683	2	Q9BAS3_9MAGN	Q9bAa3_buxus micro	1103	56	12.1	264	2	Q9CP61_PASMU	Q9cP61_pasteurella
1031	56.5	12.3	686	1	VGJH_PRIVA	P27416_pseudorabie	1104	56	12.1	274	2	Q4NIS8_9MICC	Q4niS8_athrobacte
1032	56.5	12.3	686	1	VGJH_PRIVA	Q00660_pseudorabie	1105	56	12.1	279	1	Y170_BDCBP	Q89a82_buchnera ap
1033	56.5	12.3	686	1	VGJH_PRIVA	P27593_pseudorabie	1106	56	12.1	281	2	Q7NU04_CHRYO	Q7nU04_chromobacte
1034	56.5	12.3	686	2	Q5PPA2_9ALPH	Q5pPa2_suid herpes	1107	56	12.1	282	2	Q5FT07_LACAC	Q5fT07_lactobacill
1035	56.5	12.3	688	2	Q9BAS8_9MAGN	Q9bA88_buxus henry	1108	56	12.1	283	2	Q5Z5Q1_MAGGR	Q5z5Q1_magnaporthe
1036	56.5	12.3	689	2	Q7Q3N1_ANOGA	Q7q3N1_anopheles g	1109	56	12.1	286	2	Q9CMZ4_PASMU	Q9cMz4_pasteurella
1037	56.5	12.3	690	2	Q9BAS2_9MAGN	Q9bAa2_buxus hilde	1110	56	12.1	292	2	Q9U8M8_TACTR	Q9u8M8_tachypleus
1038	56.5	12.3	690	2	Q9BAS4_9MAGN	Q9bAa4_buxus ripar	1111	56	12.1	294	2	Q6FFJ6_ACTIAD	Q6ffJ6_actinobact
1039	56.5	12.3	691	2	Q9BAO8_9MAGN	Q9bA88_buxus sempe	1112	56	12.1	295	2	Q7NFB8_GLOVI	Q7nFb8_gloeobacter
1040	56.5	12.3	692	2	Q9BAO9_9MAGN	Q9bA90_buxus gonoc	1113	56	12.1	302	2	Q7Q9G8_ANOGA	Q7q9G8_anopheles g
1041	56.5	12.3	692	2	Q9BAR0_9MAGN	Q9bAr0_buxus baiera	1114	56	12.1	304	2	Q8ESB3_OCEIH	Q8eSB3_oceanobacil
1042	56.5	12.3	692	2	Q9BAS5_9MAGN	Q9bAa5_buxus micro	1115	56	12.1	306	2	Q87HY7_VIBPA	Q87hy7_vibrio para
1043	56.5	12.3	695	2	Q9BAS7_9MAGN	Q9bAa7_buxus hartla	1117	56	12.1	319	2	Q611Y3_CAEBR	Q611y3_caenorhabdi
1044	56.5	12.3	699	2	Q96SM4_HUMAN	Q96sM4_homo sapien	1118	56	12.1	324	2	Q505K1_MOUSE	Q505k1_mus musculu
1045	56.5	12.3	704	2	Q9SC14_BUXSE	Q9sC14_buxus sempe	1119	56	12.1	325	2	Q9P487_TISNU	Q9p487_fischerella
1046	56.5	12.3	704	2	Q9BAS6_9MAGN	Q9bAa6_buxus macow	1120	56	12.1	334	2	Q52W82_9RHOD	Q52w82_rice grassy
1047	56.5	12.3	710	2	Q6C6N0_YARLI	Q6c6N0_yarrowia li	1121	56	12.1	340	2	Q504U7_HUMAN	Q504u7_homo sapien
1048	56.5	12.3	710	2	Q6C6N0_YARLI	Q6c6N0_yarrowia li	1122	56	12.1	340	2	Q8FP93_LEPIN	Q8fP93_leptospilla
1049	56.5	12.3	726	2	Q8HTM7_PODPE	Q8htM7_sinopodophy	1123	56	12.1	342	2	Q5B7Z1_EMENT	Q5b7Z1_aspergillus
1050	56.5	12.3	726	2	Q8HTM9_9MAGN	Q8hTm9_rattus norv	1124	56	12.1	344	2	Q5AMH7_EMENT	Q5aMh7_aspergillus
1051	56.5	12.3	729	2	Q5PXX6_RAT	Q5pXx6_rattus norv	1125	56	12.1	351	2	Q9BEM8_RHILLO	Q9bEm8_thizobium 1
1052	56.5	12.3	730	2	Q5PXX6_RAT	Q5pXx6_rattus norv	1126	56	12.1	352	2	Q6YT41_PIG	Q6yT41_sus scrofa
1053	56.5	12.3	757	1	KCNK3_HUMAN	Q14003_homo sapien							

1127	56	12.1	354	2	06F593_ANAPL	06F593	anas	piatyr	1200	56	12.1	568	2	04FXC6_LEIMA	04FXC6	leishmania
1128	56	12.1	359	2	05Z1Y1_NOCFA	05Z1Y1	nocardia	fa	1201	56	12.1	575	2	07N243_PHOIL	07N243	photohabu
1129	56	12.1	361	2	06Z896_ICRPU	06Z896	ictrudis	p	1202	56	12.1	576	2	07N756_PHOIL	07N756	photohabu
1130	56	12.1	363	2	08BNF7_PSEPK	08BNF7	pseudomonas		1203	56	12.1	578	1	PRF3E_RHOCA	PRF3E	r pte sybre
1131	56	12.1	364	2	05U244_HALMA	05U244	haloarcula		1204	56	12.1	581	2	08C3F7_MOUSE	08C3F7	mus musculus
1132	56	12.1	365	2	0981E3_RHILU	0981E3	rhizobium	1	1205	56	12.1	594	2	09X3S5_PSEAE	09X3S5	pseudomonas
1133	56	12.1	376	2	06CNY1_KLUIA	06CNY1	kluyveromyc		1206	56	12.1	605	2	061NM3_XENLA	061NM3	xenopus lae
1134	56	12.1	388	2	09STX2_ARATH	09STX2	arabidopsis		1207	56	12.1	610	2	076486_LEIME	076486	leishmania
1135	56	12.1	388	2	0673W2_MOUSE	0673W2	mus musculus		1208	56	12.1	621	2	04PHM6_USUMA	04PHM6	usillago ma
1136	56	12.1	398	2	07XKE3_ORYSA	07XKE3	oryza sativ		1209	56	12.1	621	2	0660P2_BORGA	0660P2	borrella ga
1137	56	12.1	405	2	07NTU3_CHRYA	07NTU3	chromobacte		1210	56	12.1	626	2	051574_BORBU	051574	borrella bu
1138	56	12.1	408	2	07PW26_ANOGA	07PW26	anopheles g		1211	56	12.1	632	2	04SUG4_TETNG	04SUG4	tetradon n
1139	56	12.1	409	2	087LM6_VIBPA	087LM6	vibrio para		1212	56	12.1	629	2	09JMA1_CLOPE	09JMA1	clostridium
1140	56	12.1	411	2	09A4V3_CAUCR	09A4V3	caulobacter		1213	56	12.1	633	2	08C415_MOUSE	08C415	mus musculus
1141	56	12.1	413	2	067T35_SYMTH	067T35	symbiodacte		1214	56	12.1	643	2	05ON53_ORYSA	05ON53	oryza sativ
1142	56	12.1	434	1	ENO_DESVM	032513	deullifovitr		1215	56	12.1	653	1	KCNH4_HUMAN	KCNH4	human
1143	56	12.1	436	1	ALBD1_BACSU	P71008	baclillus su		1216	56	12.1	690	2	073T97_MYCPA	073T97	mycobacteri
1144	56	12.1	436	1	ALBD2_BACSU	09KXG4	baclillus su		1217	56	12.1	712	2	054Q53_DICDI	054Q53	dictyostell
1145	56	12.1	438	2	09KXG4_STRCO	09KXG4	streptomyce		1218	56	12.1	724	2	08A8Y9_BACTN	08A8Y9	bacteroides
1146	56	12.1	439	2	06BRK2_DEBHA	06BRK2	debaryomyce		1219	56	12.1	736	2	028661_ARCFU	028661	archaeoglob
1147	56	12.1	440	2	08UIZ8_AGRTS	08UIZ8	agrobacteri		1220	56	12.1	752	2	04MY34_9DELT	04MY34	9delet
1148	56	12.1	442	2	0642S2_XENLA	0642S2	xenopus lae		1221	56	12.1	848	2	05ER54_9HIVI	05ER54	human
1149	56	12.1	445	2	04HBN0_9DBIO	04HBN0	delnoccus		1222	56	12.1	855	2	08A6V6_BACTN	08A6V6	bacteroides
1150	56	12.1	449	2	006407_MYCTU	006407	mycobacteri		1223	56	12.1	917	2	04WEX4_ASPFU	04WEX4	aspergillus
1151	56	12.1	449	2	07U1T6_MYCBO	07U1T6	mycobacteri		1224	56	12.1	965	2	05OLFO_9CORY	05OLFO	9corynebac
1152	56	12.1	450	2	06A6T5_PROAC	06A6T5	propionibac		1225	56	12.1	1012	2	07RCG7_PLAYO	07RCG7	plasmodium
1153	56	12.1	452	2	06DOK7_ERWCT	06DOK7	erwinia car		1226	56	12.1	1051	2	05ZPD75_ORYSA	05ZPD75	oryza sativ
1154	56	12.1	456	2	084DM6_LISMO	084DM6	liesteria mo		1227	56	12.1	1084	2	05WTH5_LSGPL	05WTH5	legionella
1155	56	12.1	456	2	084DM8_LISMO	084DM8	liesteria mo		1228	56	12.1	1118	2	06BM96_RHIME	06BM96	rhizobium m
1156	56	12.1	456	2	084DM9_LISMO	084DM9	liesteria mo		1229	56	12.1	1118	2	09Z1Y9_RHIME	09Z1Y9	rhizobium m
1157	56	12.1	457	1	DCR1B_CHICK	05Q1C3	gallus gall		1230	56	12.1	1126	2	04PEF6_USTMA	04PEF6	ustilago ma
1158	56	12.1	457	2	084DM7_LISMO	084DM7	liesteria mo		1231	56	12.1	1135	2	05X437_LSGPA	05X437	legionella
1159	56	12.1	457	2	084DM4_LISMO	084DM4	liesteria mo		1232	56	12.1	1243	2	04FRM6_9GAMM	04FRM6	9gamm
1160	56	12.1	458	2	084DN5_LISMO	084DN5	liesteria mo		1233	56	12.1	1305	1	FTEK_YERPE	FTEK	yerpe
1161	56	12.1	458	2	084DN6_LISMO	084DN6	liesteria mo		1234	56	12.1	1310	2	066CK2_YERPS	066CK2	yerps
1162	56	12.1	459	2	05FML2_XENLA	05FML2	xenopus lae		1235	56	12.1	1384	1	CNRP1_HUMAN	CNRP1	human
1163	56	12.1	461	2	084DQ5_LISMO	084DQ5	liesteria mo		1236	56	12.1	1406	2	06L3G4_SOLDE	06L3G4	solanum dem
1164	56	12.1	461	2	06ZD13_BURMA	06ZD13	burkholderi		1237	56	12.1	1439	2	07XQPI_ORYSA	07XQPI	oryza sativ
1165	56	12.1	471	2	084DQ3_LISMO	084DQ3	liesteria mo		1238	56	12.1	1462	2	081TW9_PLA7	081TW9	plasmodium
1166	56	12.1	477	2	084DM5_LISMO	084DM5	liesteria mo		1239	56	12.1	1520	2	05SUB6_CRYNS	05SUB6	cryptococcu
1167	56	12.1	477	2	084DN0_LISMO	084DN0	liesteria mo		1240	56	12.1	1608	2	059GLO_HUMAN	059GLO	human
1168	56	12.1	477	2	084DN1_LISMO	084DN1	liesteria mo		1241	56	12.1	1856	1	GBF1_CRIGR	GBF1	crigriculus
1169	56	12.1	477	2	084DN3_LISMO	084DN3	liesteria mo		1242	56	12.1	1859	1	GBF1_HUMAN	GBF1	human
1170	56	12.1	478	2	084DPO_LISMO	084DPO	liesteria mo		1243	56	12.1	1875	2	06RCQ2_LSGPN	06RCQ2	legionella
1171	56	12.1	479	2	084DP3_LISMO	084DP3	liesteria mo		1244	56	12.1	1914	2	05Z276_LSGPH	05Z276	legionella
1172	56	12.1	480	2	05Z2N7_MACGR	05Z2N7	magnaporthe		1245	56	12.1	1914	1	RLE_HUMAN	RLE	human
1173	56	12.1	488	2	04NEK3_9M1CC	04NEK3	archibactere		1246	56	12.1	1914	1	05RCL4_PONPY	05RCL4	pongy
1174	56	12.1	490	2	07N3C6_PHOIL	07N3C6	photohabu		1247	56	12.1	2055	1	MPDZ_MOUSE	MPDZ	mouse
1175	56	12.1	494	2	05V4M5_HALMA	05V4M5	haloarcula		1248	56	12.1	3972	2	07PMJ6_ANOGA	07PMJ6	anoga
1176	56	12.1	503	1	VLI_HPV32	P36737	human papil		1249	56	12.1	6994	2	017343_CABEL	017343	cabel
1177	56	12.1	503	1	05N550_SYNPG	05N550	synecbococ		1250	56	12.1	6994	2	017490_CABEL	017490	cabel
1178	56	12.1	508	2	08FP11_CONEF	08FP11	corynebacte		1251	55.5	12.0	62	2	08CKT3_YERPE	08CKT3	yerpe
1179	56	12.1	516	2	08CE47_MOUSE	08CE47	mus musculu		1252	55.5	12.0	63	2	04FLU9_9RICK	04FLU9	9rick
1180	56	12.1	516	2	094M77_CTEFR	094M77	ctenogobio		1253	55.5	12.0	84	2	05WGD8_BACSK	05WGD8	bacsk
1181	56	12.1	518	2	04IHP5_GIBZE	04IHP5	gibberella		1254	55.5	12.0	124	2	08BL31_PSEPK	08BL31	psepk
1182	56	12.1	519	2	09VXK1_DROME	09VXK1	drosophila		1255	55.5	12.0	134	2	06FSR7_BACCE	06FSR7	bacce
1183	56	12.1	524	2	081AE6_BACCR	081AE6	baclillus ce		1256	55.5	12.0	138	2	05TLT8_MOUSE	05TLT8	mouse
1184	56	12.1	525	2	04RM80_TETNG	04RM80	tetradon n		1257	55.5	12.0	141	2	06YXR7_PHYPA	06YXR7	phyecomit
1185	56	12.1	528	2	04KCT5_PSEF5	04KCT5	pseudomonas		1258	55.5	12.0	147	2	063K49_BURPS	063K49	burkholderi
1186	56	12.1	531	2	041973_GIBZE	041973	gibberella		1259	55.5	12.0	147	2	06ZB21_BURMA	06ZB21	burkholderi
1187	56	12.1	539	1	CH60_EBTAG	066026	enterobacte		1260	55.5	12.0	151	2	08BDH7_VIBVO	08BDH7	vibrio vuln
1188	56	12.1	539	1	CH60_EBTAS	066190	enterobacte		1261	55.5	12.0	157	2	093287_BROIN	093287	bromus iner
1189	56	12.1	540	1	CH60_KLEOR	066210	klebsiella		1262	55.5	12.0	168	2	06U398_LACPL	06U398	lactobacilli
1190	56	12.1	540	1	CH60_KLEOX	066210	klebsiella		1263	55.5	12.0	177	2	04LXV9_9BURK	04LXV9	9burkholderi
1191	56	12.1	544	1	CH60_AERSA	068309	aeromonas s		1264	55.5	12.0	179	2	06LME1_PROPR	06LME1	photobacter
1192	56	12.1	545	2	06TLJ7_9PSEBD	06TLJ7	pseudomonas		1265	55.5	12.0	184	2	07BKF5_PROB01	07BKF5	gamma-prote
1193	56	12.1	547	2	CH60_KLEPN	066026	klebsiella		1266	55.5	12.0	186	2	08JUM5_SHIFL	08JUM5	shigella fl
1194	56	12.1	547	2	09Z2B8_RHIME	09Z2B8	rhizobium m		1267	55.5	12.0	186	2	05W7K0_XENTR	05W7K0	xenopus tro
1195	56	12.1	548	2	06YXK3_XENNE	06YXK3	xenorhabdus		1268	55.5	12.0	187	2	0707B6_XENOL	0707B6	escherichia
1196	56	12.1	557	1	PMO4_HUMAN	P31512	homo sapien		1269	55.5	12.0	187	2	08CVQ9_ECOLI	08CVQ9	ecol
1197	56	12.1	557	1	05RDN6_PONPY	P31512	pongo pygma		1270	55.5	12.0	191	2	06E5S2_FUGRU	06E5S2	fugu rubrip
1198	56	12.1	558	2	053XR0_HUMAN	053XR0	homo sapien		1271	55.5	12.0	194	1	TM22_HUMAN	TM22	human
1199	56	12.1	559	2	06UN75_TOBAC	06UN75	nicotiana t		1272	55.5	12.0	196	1	CLPPI1_PROMP	CLPPI1	promp

1273	55.5	12.0	198	2	Q87A07_XYLFT	Q87A07_xylfella fas	1346	55.5	12.0	382	2	Q5B1P0_BOVIN	Q5B1P0_bos taurus
1274	55.5	12.0	199	2	Q65D47_BACLD	Q65d47 bacillus li	1347	55.5	12.0	383	1	YJUK8_YEAST	P2946 saccharomyc
1275	55.5	12.0	206	2	Q9SE77_BRAOL	Q9se77 brassica oi	1348	55.5	12.0	383	2	Q6O5N7_YEAST	Q6546 saccharomyc
1276	55.5	12.0	211	2	Q9NA02_9CRUS	Q9na02 daphnia mag	1349	55.5	12.0	383	2	Q5Z0K5_NOCFA	Q520K5 nocardia fa
1277	55.5	12.0	213	2	Q9NA09_CABEL	Q9na09 caenorhabdi	1350	55.5	12.0	384	2	Q9L1J8_BRANA	Q9L1J8 brassica fa
1278	55.5	12.0	214	2	Q61ZM4_CABER	Q61zm4 caenorhabdi	1351	55.5	12.0	384	2	Q9L1A9_ARATH	Q9L1A9 arabidopsis
1279	55.5	12.0	221	2	Q6CL37_KUULA	Q6cl37 kluyveromyc	1352	55.5	12.0	385	2	Q9FX15_ARATH	Q9FX15 arabidopsis
1280	55.5	12.0	223	2	Q9DCP4_MOUSE	Q9dcp4 mus musculu	1353	55.5	12.0	389	2	Q6PQJ8_DIGPU	Q6pqj8 digitealis p
1281	55.5	12.0	232	2	Q8B5R5_9TOMB	Q8b5r5 beet black	1354	55.5	12.0	389	2	Q5HVY0_CAMJR	Q5hv0 campylobact
1282	55.5	12.0	235	2	Q4LOA6_9BURK	Q4loa6 burkholderi	1355	55.5	12.0	389	2	Q9PPF7_CAMJR	Q9ppf7 campylobact
1283	55.5	12.0	237	2	Q419H8_GIBZE	Q419h8 gibberella	1356	55.5	12.0	393	2	Q4NU11_9DELT	Q4nu11 anaeromycob
1284	55.5	12.0	237	2	Q4ZOA9_PSESY	Q4zoa9 pseudomonas	1357	55.5	12.0	394	2	Q56OQ3_CRYNE	Q56oq3 cryptococcu
1285	55.5	12.0	237	2	Q8B5Y3_PSEBSM	Q8b5y3 pseudomonas	1358	55.5	12.0	407	2	Q94Y7C6_TRIMO	Q947c6 triticum mo
1286	55.5	12.0	240	2	Q8XW05_RALSO	Q8xw05 ralsstonia s	1359	55.5	12.0	409	2	Q4NRD2_9DELT	Q4nrd2 anaeromycob
1287	55.5	12.0	245	2	Q98R89_MYCPVU	Q98r89 mycoplasma s	1360	55.5	12.0	414	2	Q7MHX0_VIBVY	Q7mhd0 vibrio vuln
1288	55.5	12.0	245	2	Q7ZYWI_BARRI	Q7zywi brachydantio	1361	55.5	12.0	417	2	Q9Z1S3_ECOLI	Q9z1s3 escherichia
1289	55.5	12.0	248	2	Q6CA49_YARLI	Q6ca49 yarrowia li	1362	55.5	12.0	425	2	Q5WRJ3_LEGFL	Q5wrj3 legionella
1290	55.5	12.0	250	2	Q8B147_BRARJ	Q8b147 bradyrhizob	1363	55.5	12.0	425	2	Q5WXT6_LEGFL	Q5wxt6 legionella
1291	55.5	12.0	253	2	Q7PJ20_ANOGS	Q7pj20 anopheles g	1364	55.5	12.0	425	2	Q5X6C6_LEGPA	Q5x6c6 legionella
1292	55.5	12.0	253	2	Q8FP86_COREF	Q8fp86 corynebacte	1365	55.5	12.0	431	2	Q9MS90_9MAGN	Q9ms90 austroballe
1293	55.5	12.0	254	2	Q9RWP1_DEIRA	Q9rwp1 deinococcus	1366	55.5	12.0	437	2	Q83CE5_COXBU	Q83ce5 coxiella bu
1294	55.5	12.0	256	2	Q9RUK4_DEIRA	Q9ruk4 deinococcus	1367	55.5	12.0	451	2	Q4NMW3_9DELT	Q4nmw3 anaeromycob
1295	55.5	12.0	257	1	PEBB_PROMW	Q7585 prochloroxo	1368	55.5	12.0	452	2	Q8KX57_CHLRE	Q8kx57 chlorobium
1296	55.5	12.0	262	1	BACR_HALSA	P02945 halobacteri	1369	55.5	12.0	456	2	Q2O5J3_CABEL	Q2o5j3 caenorhabdi
1297	55.5	12.0	262	2	Q5HLT2_STAEQ	Q5hl12 streptyllocc	1370	55.5	12.0	459	2	Q9C1K1_LACLA	Q9c1k1 lactococcus
1298	55.5	12.0	262	2	Q4G5W6_BRARE	Q4g5w6 brachydantio	1371	55.5	12.0	470	2	Q7MSR1_WOLUX	Q7msr1 wolfinella s
1299	55.5	12.0	263	2	Q5CVY7_CRYPV	Q5cvy7 cryptospori	1372	55.5	12.0	471	2	Q5FT20_GLUOX	Q5ft20 glucinobact
1300	55.5	12.0	263	2	Q5CFK0_CRYHO	Q5cfk0 cryptospori	1373	55.5	12.0	483	2	Q91B29_ONCMY	Q91b29 oncorhynch
1301	55.5	12.0	270	2	Q5YUJ0_HUMAN	Q5yu10 homo sapien	1374	55.5	12.0	484	2	Q4ZCR7_9VIRU	Q4zcr7 bacteriophu
1302	55.5	12.0	270	2	Q98R66_BRARE	Q98r66 brachydantio	1375	55.5	12.0	484	2	Q7JRS3_TREDE	Q7jrs3 treponema d
1303	55.5	12.0	283	2	Q5V2V1_HALMA	Q5v2v1 haloarcula	1376	55.5	12.0	484	2	Q8NM17_STAMW	Q8nm17 streptom d
1304	55.5	12.0	292	2	Q91XR2_CAVPO	Q91xr2 cavia porce	1377	55.5	12.0	516	2	Q5JBB0_9LILI	Q5jbb0 toxiscord
1305	55.5	12.0	295	2	Q6G6NT_XENLA	Q6g6nt xenopus lae	1378	55.5	12.0	522	2	Q8D5G2_VIBVU	Q8d5g2 vibrio vuln
1306	55.5	12.0	299	2	Q9H218_PSEAE	Q9h218 pseudomonas	1379	55.5	12.0	522	2	Q7MCQ9_VIBVU	Q7mcq9 vibrio vuln
1307	55.5	12.0	300	2	Q5P736_AZOSB	Q5p736 azococcus sp	1380	55.5	12.0	528	2	Q7JKN6_TREDE	Q7jkn6 treponema d
1308	55.5	12.0	309	2	Q8DPP1_STRR6	Q8dpp1 streptococc	1381	55.5	12.0	528	2	Q4RJ06_TRENG	Q4rj06 treponema n
1309	55.5	12.0	309	2	Q97QL2_STRPN	Q97ql2 streptococc	1382	55.5	12.0	529	2	Q5CP72_CRYHO	Q5cp72 cryptospori
1310	55.5	12.0	312	1	CATO_MOUSE	Q8bm88 mus musculu	1383	55.5	12.0	545	2	Q8PYL8_ANASP	Q8pyl8 anabeana sp
1311	55.5	12.0	312	1	Q4QQL3_MOUSE	Q4qq13 mus musculu	1384	55.5	12.0	545	2	Q9PXA4_9PARA	Q9pxa4 mearesia vir
1312	55.5	12.0	315	2	Q6LHU3_PHOPR	Q6lhu3 photobacter	1385	55.5	12.0	546	2	Q91HA5_9PARA	Q91ha5 reidreast
1313	55.5	12.0	316	2	Q9RUA8_DEIRA	Q9rua8 deinococcus	1386	55.5	12.0	553	2	Q113B0_9PARA	Q113b0 mearesia vir
1314	55.5	12.0	317	1	EXOZ_RHIME	P25502 rhizobium m	1387	55.5	12.0	562	1	Y3471_BRARJ	Y3471 brachyryzob
1315	55.5	12.0	323	2	Q888H6_PSESM	Q888h6 pseudomonas	1388	55.5	12.0	566	2	Q5H4R5_XANOR	Q5h4r5 xanthomonas
1316	55.5	12.0	324	2	Q9BF55_ATEFU	Q9bf55 ateleis fusc	1389	55.5	12.0	572	2	Q5R773_PONPY	Q5r773 pongo pygma
1317	55.5	12.0	325	2	Q6LG56_PHOPR	Q6lg56 photobacter	1390	55.5	12.0	580	2	Q98DA6_RHIL0	Q98da6 rhizobium l
1318	55.5	12.0	326	2	Q97CS8_THIEVO	Q97cs8 thermoplasma	1391	55.5	12.0	587	2	Q9FKO5_ARATH	Q9fk05 arabidopsis
1319	55.5	12.0	326	2	Q9BF60_PIG	Q9bf60 sus scrofa	1392	55.5	12.0	595	2	Q5RSH6_PONPY	Q5rsh6 pongo pygma
1320	55.5	12.0	326	2	Q9BF60_LEMCA	Q9bf60 lemur catla	1393	55.5	12.0	595	2	Q7NJB4_GLOVY	Q7njb4 gloebacter
1321	55.5	12.0	326	2	Q9BF72_SORAR	Q9bf72 sotex arane	1394	55.5	12.0	607	2	Q9CY11_ARATH	Q9cy11 arabidops
1322	55.5	12.0	326	2	Q9BF75_MYRTR	Q9bf75 myrmecophag	1395	55.5	12.0	625	1	KCNCA4_RAT	KCNCA4 rat
1323	55.5	12.0	326	2	Q9BF76_TAMTE	Q9bf76 tamandua te	1396	55.5	12.0	628	1	KCNCA4_MOUSE	KCNCA4 mouse
1324	55.5	12.0	326	2	Q99NQ7_ACOGA	Q99nq7 agouti tacz	1397	55.5	12.0	631	2	Q7VND5_HAEUD	Q7vnd5 haemophilus
1325	55.5	12.0	326	2	Q99NQ9_HYDHY	Q99nq9 hydrochoeru	1398	55.5	12.0	631	2	Q803A6_BRARE	Q803a6 brachydantio
1326	55.5	12.0	326	2	Q99NR0_9HYST	Q99nr0 cavia teschu	1399	55.5	12.0	634	2	Q96LJ0_DROME	Q96lj0 drosophiila
1327	55.5	12.0	326	2	Q99NR3_EREDO	Q99nr3 erethizon d	1400	55.5	12.0	635	1	KCNCA4_HUMAN	KCNCA4 homo sapien
1328	55.5	12.0	326	2	Q99NR4_HYSBR	Q99nr4 hyestrix bra	1401	55.5	12.0	643	1	YKDE_CABEL	YKDE caenorhabdi
1329	55.5	12.0	326	2	Q99NR8_CASCN	Q99nr8 castor cana	1402	55.5	12.0	648	1	HEPA_HHY6U	HEPA human herpe
1330	55.5	12.0	331	2	Q59NG2_CANAL	Q59ng1 candida alb	1403	55.5	12.0	662	1	PEPS_ORYSA	PEPS2375 human
1331	55.5	12.0	331	2	Q5KPG4_CRYNE	Q5kpg4 cryptococcu	1404	55.5	12.0	678	2	Q9BXR8_HUMAN	Q9bxr8 homo sapien
1332	55.5	12.0	336	2	Q4H4M1_9DEIO	Q4h4m1 deinococcus	1405	55.5	12.0	687	2	Q82F42_STRAM	Q82f42 streptomyc
1333	55.5	12.0	341	2	Q4H4Z8_9DEIO	Q4h4z8 deinococcus	1406	55.5	12.0	698	2	Q84Z10_ORYSA	Q84z10 oryza sativ
1334	55.5	12.0	343	2	Q98R65_BRARE	Q98r65 brachydantio	1407	55.5	12.0	716	1	P5CS_ORYSA	P5CS2775 oryza sativ
1335	55.5	12.0	344	2	Q8YQJ5_ANASP	Q8yqj5 anabaena sp	1408	55.5	12.0	716	1	Q6PW76_ORYSA	Q6pw76 oryza sativ
1336	55.5	12.0	346	2	Q59293_PYRHO	Q59293 pyrococcus	1409	55.5	12.0	716	2	Q6OEM4_ORYSA	Q6oem4 oryza sativ
1337	55.5	12.0	346	2	Q74ON5_MYCPA	Q74on5 mycobacteri	1410	55.5	12.0	726	2	Q8HTM8_9MAGN	Q8htm8 diphylla
1338	55.5	12.0	357	2	Q8Q1T8_NYVAH	Q8q1t8 adoxophyes	1411	55.5	12.0	740	2	Q8DU17_SYNBL	Q8du17 synethococc
1339	55.5	12.0	358	2	Q6TTC7_SYWTH	Q6ttc7 symbiodacte	1412	55.5	12.0	742	2	Q6MNV6_BDEBA	Q6mnv6 bdellovibri
1340	55.5	12.0	376	1	OE56_NPVAC	P41705 autographa	1413	55.5	12.0	751	2	Q9AYM4_VIGUN	Q9aym4 vigna ungui
1341	55.5	12.0	378	1	Q8B9B5_NPVRO	Q8b9b5 rechipluteia	1414	55.5	12.0	788	2	Q6INE9_XENLA	Q6ine9 xenopus lae
1342	55.5	12.0	379	1	OE56_NPVCF	P41718 chorioloneu	1415	55.5	12.0	806	1	PAZG6_HUMAN	PAZG6 homo sapien
1343	55.5	12.0	379	2	Q8B2F2_PSESM	Q8b2f2 pseudomonas	1416	55.5	12.0	806	2	Q7MWV0_BORPA	Q7mwv0 bordetella
1344	55.5	12.0	379	2	Q77DF6_NPVCF	Q77df6 chorioloneu	1417	55.5	12.0	806	2	Q7MP30_BORBR	Q7mp30 bordetella
1345	55.5	12.0	381	2	Q8ZB18_STRAM	Q8zb18 streptomyc	1418	55.5	12.0	806	2	Q7MP30_VIBVY	Q7mp30 vibrio vuln

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1419 55.5 12.0 849 2 QARGD7 TETNG
1420 55.5 12.0 880 2 Q4RM12 BRARE
1421 55.5 12.0 886 1 SEM6B MOUSE
1422 55.5 12.0 887 1 SEM6B_RAT
1423 55.5 12.0 888 1 SEM6B_HUMAN
1424 55.5 12.0 893 1 DAQ1_MOUSE
1425 55.5 12.0 893 2 Q8BPJ7 MOUSE
1426 55.5 12.0 893 2 Q8CB6F MOUSE
1427 55.5 12.0 893 2 Q544G5 MOUSE
1428 55.5 12.0 895 1 DAQ1_BOVIN
1429 55.5 12.0 925 1 Q7XPE9 ORYSA
1430 55.5 12.0 946 1 C1TC_YEAST
1431 55.5 12.0 968 2 Q8TW58 METKA
1432 55.5 12.0 1020 2 Q95XY4 CAEBL
1433 55.5 12.0 1062 2 Q7OV26 GIALA
1434 55.5 12.0 1104 2 Q7S728 NEUCR
1435 55.5 12.0 1119 2 Q5BA79 EBENI
1436 55.5 12.0 1131 2 Q6C011 YARLI
1437 55.5 12.0 1148 2 Q54YC9 DICDI
1438 55.5 12.0 1217 2 Q17889 CAEBL
1439 55.5 12.0 1423 1 FRUA_STRMU
1440 55.5 12.0 1453 2 Q7TET3 SCORO
1441 55.5 12.0 1469 2 Q4WTA3 ASPFU
1442 55.5 12.0 1632 2 Q4SID3 TETNG
1443 55.5 12.0 1637 2 Q5O297 ENTHI
1444 55.5 12.0 1731 2 Q4OJ23 LEIMA
1445 55.5 12.0 1913 2 Q4Q986 LEIMA
1446 55.5 12.0 2054 1 MPD2_RAT
1447 55.5 12.0 2220 2 Q9GV40 DROME
1448 55.5 12.0 2236 2 Q9VCN1 DROME
1449 55.5 12.0 4905 2 Q4FE23 LEIMA
1450 55.5 11.9 52 2 Q4S059 CAEBL
1451 55.5 11.9 66 2 Q7UB8Y3 SYNAPX
1452 55.5 11.9 92 2 Q4RYG8 TERNX
1453 55.5 11.9 93 2 Q82Q38 STRAW
1454 55.5 11.9 94 2 Q8SP51 9CUCU
1455 55.5 11.9 95 2 Q864R3 CANFA
1456 55.5 11.9 123 2 Q6LGG8 PHCPR
1457 55.5 11.9 128 1 Y070_TREPA
1458 55.5 11.9 134 2 Q86ZV1 NEUCR
1459 55.5 11.9 159 2 Q5XD59 STRP6
1460 55.5 11.9 159 2 Q9A0V4 STRP6
1461 55.5 11.9 159 2 Q7CNF4 STRP8
1462 55.5 11.9 159 2 Q7CPB9 STRP3
1463 55.5 11.9 160 1 P8TD_GDTH
1464 55.5 11.9 166 2 Q5Q8S5 PHATA
1465 55.5 11.9 178 1 CRCB2_BIFLO
1466 55.5 11.9 190 2 Q6W3A0 9CREN
1467 55.5 11.9 202 2 Q62KV1 BURMA
1468 55.5 11.9 202 2 Q63TK1 BURPS
1469 55.5 11.9 208 2 Q9PS81 CHICK
1470 55.5 11.9 212 2 Q8B874 VIBVU
1471 55.5 11.9 212 2 Q9KGG3 VIBCH
1472 55.5 11.9 218 2 Q848N7 9BACT
1473 55.5 11.9 220 2 Q841E1 BACFR
1474 55.5 11.9 223 2 Q9XCA4 PORGI
1475 55.5 11.9 225 2 Q9BRQ7 HUMAN
1476 55.5 11.9 228 2 Q83UY3 LISMO
1477 55.5 11.9 228 2 Q63R53 BURPS
1478 55.5 11.9 229 2 Q62HE2 BURMA
1479 55.5 11.9 229 2 Q83TM3 LISMO
1480 55.5 11.9 229 2 Q83UH3 LISMO
1481 55.5 11.9 235 2 Q8NC40 HUMAN
1482 55.5 11.9 235 2 Q7MM99_VIBV
1483 55.5 11.9 242 2 Q9BSV0 HUMAN
1484 55.5 11.9 252 2 Q6LUV0 PODAN
1485 55.5 11.9 252 2 Q7TNC3 MOUSE
1486 55.5 11.9 253 2 Q63I01 BURPS
1487 55.5 11.9 255 2 Q8TUS5 METKA
1488 55.5 11.9 263 2 Q8GPE8 STRAU
1489 55.5 11.9 263 2 Q79HD6_FRAIT
1490 55.5 11.9 264 2 Q6Z3B6 ORYSA
1491 55.5 11.9 265 2 Q7PIL4_CHRVO

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Q4RGD7 tetraodon n
Q4RM12 brachydanio
Q54951 mus musculus
Q70141 rattus norv
Q931c3 homo sapien
Q62165 mus musculu
Q8BPJ7 mus musculu
Q8CB6F mus musculu
Q544G5 mus musculu
Q18738 bos taurus
Q7XPE9 oryza sativ
P07245 s c-1-tetra
Q8TW58 mechanopyru
Q95XY4 caenorhabdi
Q7GV26 giardia lam
Q7S728 neurospora
Q5BA79 aspergillus
Q6C011 yarrowia li
Q54YC9 dictyosteli
Q17889 caenorhabdi
Q03174 streptococc
Q7TET3 canine coro
Q4WTA3 aspergillus
Q4SID3 tetraodon n
Q5O297 entamoeba h
Q4OJ23 leishmania
Q4Q986 leishmania
Q53164 rattus norv
Q9GV40 dirosophila
Q9VCN1 dirosophila
Q4FE23 leishmania
Q4S059 caenorhabdi
Q7UB8Y3 synchococc
Q4RYG8 tetraodon n
Q82Q38 streptomyce
Q8SP51 oclorhynchu
Q864R3 canis famli
Q6LGG8 threponema p
Q83109 treponema p
Q86ZV1 neutrospora
Q5XD59 streptococc
Q9A0V4 streptococc
Q7CNF4 streptococc
Q7CPB9 streptococc
Q78451 guillardia
Q5Q8S5 phaeogale
Q8G5C3 bitidobacte
Q6W3A0 uncultured
Q62KV1 burkholderi
Q63TK1 burkholderi
Q9PS81 gallus gall
Q8B874 vibrio vuln
Q9KGG3 vibrio chol
Q848N7 uncultured
Q841E1 bacteroides
Q9XCA4 porphyromon
Q9BRQ7 homo sapien
Q83UY3 listeria mo
Q63R53 burkholderi
Q62HE2 burkholderi
Q83TM3 listeria mo
Q83UH3 listeria mo
Q8NC40 homo sapien
Q7MM99 vibrio vuln
Q9BSV0 homo sapien
Q6LUV0 podospora a
Q7TNC3 mus musculu
Q63I01 burkholderi
Q8TUS5 methanopyru
Q8GPE8 streptomyce
Q79HD6 francisella
Q6Z3B6 oryza sativ
Q7PIL4 chromobacte

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1492 55 11.9 268 1 EA30_VICFA
1493 55 11.9 268 2 Q43675 VICFA
1494 55 11.9 270 2 Q94006 CANAL
1495 55 11.9 270 2 Q5A4M8 CANAL
1496 55 11.9 270 2 Q8BY38_MOUSE
1497 55 11.9 273 2 Q73NN2_TREDE
1498 55 11.9 275 2 Q54KD4_DICDI
1499 55 11.9 277 2 Q9FYE3_ARATH
1500 55 11.9 282 2 Q9Y4U1_HUMAN

ALIGNMENTS

RESULT 1
Q6UWZ1 HUMAN PRELIMINARY; PRT; 89 AA.
ID Q6UWZ1;
AC Q6UWZ1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE BRV526
GN Name=FXID4; ORFNames=UNQ526;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2288796; PubMed=12975109; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie B., Sanchez C., Schenfeld J.,
RA Seshagiri L., Simmon L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
RA Yandura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatic assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL: AY358584; AA088947.1; -, mRNA.
DR HGNC: HGNC:4028; FXID4.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005216; P:ion channel activity; IEA.
DR GO: GO:0006811; P:ion transport; IEA.
DR InterPro: IPR000272; FXYD.
DR Pfam: PF02038; ATP1G_PLM_MAT8; 1.
DR PROSITE: PS01310; FXYD; 1.
SQ
SEQUENCE 89 AA; 9433 MW; CS93428018244980 CRC64;

Query Match 100.0%; Score 461; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 3e-41;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALLLGLTALRANRPFANKDPFYDWNKQLQSLGICGLAIAGIAVLSGK 60
DB 1 MERVTLALLLGLTALRANRPFANKDPFYDWNKQLQSLGICGLAIAGIAVLSGK 60

QY 61 CKYKSSQKHSPVPEKATPLTPGSAATTC 89
DB 61 CKYKSSQKHSPVPEKATPLTPGSAATTC 89

RESULT 2
Q7Z4M5 HUMAN PRELIMINARY; PRT; 89 AA.
ID Q7Z4M5;
AC Q7Z4M5;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

```

DT 13-SEP-2005 (TrEMBL:rel. 31, Last annotation update)
 DE FXD domain containing ion transport regulator 4.
 GN Name=FXD4; ORFNames=Rpl1-92P6.2-004;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 CC Homo.
 NCBI_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney.
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Abramson R.D., Mullaly S.J.,
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Strauberg R.;
 RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Corby N.;
 RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC054876; AAH54876.1; -; mRNA.
 DR EMBL; AL512654; CA117065.1; -; Genomic DNA.
 DR Ensemble; ENSG00000150201; Homo sapiens.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR InterPro; IPR000272; FYXD.
 DR Pfam; PF02038; ATP1G1_PLM_MAT8.1.
 DR PROSITE; PS01310; FYXD.1.
 DR SEQUENCE 89 AA; 9373 MW; C595929A2449B0 CRC64;
 SQ
 Query Match 98.0%; Score 452; DB 2; Length 89;
 Best local similarity 98.9%; Pred. No. 2.7e-40;
 Matches 88; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 MERVTLALLLAGTALFANDPFANKDDPFYDWMKNLQSLGICGLAIAVAVSGK 60
 Db 1 MERVTLALLLAGTALFANDPFANKDDPFYDWMKNLQSLGICGLAIAVAVSGK 60
 Oy 61 CKYSSQKOHSPVPEKAIPLITPGSATTC 89
 Db 61 CKYSSQKOHSPVPEKAIPLITPGSATTC 89
 RESULT 3
 FXD4_HUMAN STANDARD; PRT; 89 AA.
 AC P59646;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXD domain-containing ion transport regulator 4 precursor.

GN Name=FXD4;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 CC Homo.
 NCBI_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Abramson R.D., Mullaly S.J.,
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
 RX MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
 RA Sweadner K.J., Rael E.;
 RT "The FXD gene family of small ion transport regulators or channels:
 RT cDNA sequence, protein signature sequence, and expression.";
 RL Genomics 68:41-56(2000).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
 CC -1- SIMILARITY: Belongs to the FXD family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; A182935; -; NOT ANNOTATED CDS; mRNA.
 CC Ensemble; ENSG00000150201; Homo sapiens.
 DR HGN; HGNC:4028; FXD4.
 DR InterPro; IPR000272; FYXD.
 DR Pfam; PF02038; ATP1G1_PLM_MAT8.1.
 DR PROSITE; PS01310; FYXD.1.
 KW Ion transport; Ionic channel; Signal; Transmembrane; Transport.
 FT SIGNAL 1 20
 FT CHAIN 21 89
 FT TOPO_DOM 21 38
 FT TRANSMEM 39 59
 FT TOPO_DOM 60 89
 SQ SEQUENCE 89 AA; 9373 MW; B595EP9A949B4 CRC64;
 Query Match 97.6%; Score 450; DB 1; Length 89;
 Best local similarity 97.8%; Pred. No. 4.5e-40;
 Matches 87; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 MERVTLALLLAGTALFANDPFANKDDPFYDWMKNLQSLGICGLAIAVAVSGK 60
 Db 1 MERVTLALLLAGTALFANDPFANKDDPFYDWMKNLQSLGICGLAIAVAVSGK 60
 Oy 61 CKYSSQKOHSPVPEKAIPLITPGSATTC 89
 Db 61 CKYSSQKOHSPVPEKAIPLITPGSATTC 89

RESULT 4
 FXD4 MOUSE STANDARD; PRT; 88 AA.
 ID FXD4 MOUSE
 AC 092070
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXD domain-containing ion transport regulator 4 precursor (Channel inducing factor) (CHIF).
 GN Name=FXD4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 CC NCBI_TaxId=10090;
 CX [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SvJ;
 RA Garty H.;
 RT "Genomic sequence of mouse CHIF (FXD4).";
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi I., Bono H., Kondo S., Naito I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Karpman A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chochia A., Corbali L.E., Cousins S., Dalia E., Dregan T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaesteland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grummond S., Gustincich S., Hitokawa N., Jackson J.J., Jarvis E.D., Kawai A., Kawaji H., Kawasawa Y., Kedierski R.M., King B.L., Kozmaga D.R., Maltale L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numa K., Okido T., Pavan W.J., Perera G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandell A., Schneider C., Sempke C.A., Seton M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang L., Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carrinci P., Hayatsu N., Hitotake K., Kikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Shitake T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Stensberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Abramson R.D., Mallory S.J., Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallory S.J., Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A., Whaley J., Helton E., Ketteman M., Madan A., Rodighiero S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Kizyinski M.I., Skalska U., Smailus D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC CC
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the FXD family.
 CC CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL: AF362729; AAK51508.1; -; Genomic DNA.
 CC EMBL: AK018728; BAB31372.1; -; mRNA.
 CC EMBL: BC086918; AAB86918.1; -; mRNA.
 CC EMBL: ENSMUSG0000004988; Mus musculus.
 CC MGI: MGI:189005; Fxd4.
 CC GO: GO:0005615; C:extracellular space; TAS.
 CC GO: GO:0016021; C:integral to membrane; TAS.
 CC InterPro: IPR000272; Fxd4.
 CC Pfam: PF02038; ATP1C1_PLM_MAT8; 1.
 CC DR PROSITE: PS01310; Fxd4; 1.
 CC Ion transport; Ion channel; Signal; Transmembrane; Transport.
 CC FT SIGNAL 1 20
 CC CHAIN 1 28
 CC FT TOPO DOM 21 38
 CC FT TRANSM 39 59
 CC FT TOPO DOM 60 88
 CC SQ SEQUENCE 88 AA; 9269 MW; 7EB0140941CFE926 CRC64;
 Query Match 60.0%; Score 276.5; DB 1; Length 88;
 Best Local Similarity 66.7%; Pred. No. 1.4e-21;
 Matches 60; Conservative 8; Mismatches 19; Indels 3; Gaps 3;
 Oy 1 MERVTLA-LLTLAGTALTEADPFANRDPFYDWMKNTLSGLTICGMLAIAVAVSG 59
 Db 1 MEIRICALLLLAGPALAEADP-VKDSFYDWSIQGLIFGGLCTAGIMAVLSG 59
 Oy 60 KCKYKSSQKQSHSPVEKAIPLTPGSARTC 89
 Db 60 KCKCRTRHKP-SLPGKATPLIPGSANTC 88
 RESULT 5
 FXD4 RAT STANDARD; PRT; 87 AA.
 ID FXD4 RAT
 AC 063113;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXD domain-containing ion transport regulator 4 precursor (Channel inducing factor) (CHIF) (Corticosteroid-induced protein).
 GN Name=FXD4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
 CC NCBI_TaxId=10116;
 CX [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Miscar; TISSUE=Colon;
 RX MEDLINE=95320221; PubMed=7597086;
 RA Attali B., Latier H., Rachamin N., Garty H.;
 RT "A corticosteroid-induced gene expressing an 'Isk-like' K+ channel activity in Xenopus oocytes."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:6092-6096(1995).
 [2]
 RP TISSUE SPECIFICITY.
 RC MEDLINE=9700648; PubMed=8843704;
 RA Caputo C., Couty N., Bonvalet J.-P., Becoubet B., Garty H.,

QY 1 MERVTLALL-LLAGLTALBANDPFANKDDPFYDMKQLQSLGICGGLAIGIAAVLSG 59
 DB 1 MGEVLSLVLLVLAGLPTLDANDP-ENKNDPFYDMWLSLVGGLICGGLAIGIIVLWSG 59
 QY 60 KCKYKSSQKOHSPVPEKAIPLITPGSATTG 89
 DB 60 KCKCKFRQKP-SHRPGEGBPLITPGSAHNC 88

RESULT 7
 ID FXD3_RAT STANDARD; PRT; 88 AA.
 AC P59645;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXD domain-containing ion transport regulator 3 precursor.
 OS Name=FXD3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN NUCLEOTIDE SEQUENCE.
 RP Lee N.H., Glodek A., Chandra I., Mason T.M., Quackenbush J.,
 RA Kerlavage A.R., Adams M.D., EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RX RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
 RP MEDLINE=20408885; PubMed=10950925; DOI=10.1006/geno.2000.6274;
 RA Sweadner K.J., Rael E.;
 RT "The FXD gene family of small ion transport regulators or channels:
 CC CDNA sequence, protein signature sequence, and expression.";
 RL Genomics 68:41-56(2000).
 CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current
 CC when expressed in Xenopus oocytes. May be a modulator capable of
 CC activating endogenous oocyte channels.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the FXD family.
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AA013165; -; NOT ANNOTATED CDS; mRNA.
 DR Ensemble; ENSRNOG0000021095; Rattus norvegicus.
 DR InterPro; IPR000272; FXD.
 DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
 DR PROSITE; PS01310; FXD; 1.
 KW Ion transport; Ionic channel; Signal; Transmembrane; Transport.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 88 FXD domain-containing ion transport
 FT regulator 3.
 FT TOPO_DOM 21 38 Extracellular (Potential).
 FT TRANSMEM 39 59 Potential.
 FT TOPO_DOM 60 88 Cytoplasmic (Potential).
 SQ SEQUENCE 88 AA; 9411 MW; 45AFEB72FDIAF944 CRC64;

Query Match 50.9%; Score 234.5; DB 1; Length 88;
 Best Local Similarity 56.7%; Pred. No. 4,2e-17;
 Matches 51; Conservative 10; Mismatches 26; Indels 3; Gaps 3;

RESULT 8
 ID FXD3_PIG STANDARD; PRT; 88 AA.
 AC O97797;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXD domain-containing ion transport regulator 3 precursor (Chloride
 DE conductance inducer protein Mac-8) (Mammary tumor 8 Kda protein).
 GN Name=FXD3; Synonyms=Mat8;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 NC NCB1_TaxID=9823;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=GASTRIC MUCOSA;
 RX MEDLINE=99140476; PubMed=10206733;
 RA Maeda M., Hamano K., Hirano Y., Suzuki M., Takahashi E.-I., Terada T.,
 RA Futai M., Sato R.;
 RT "Structures of P-type transporting ATPases and chromosomal locations
 RT of their genes.";
 RL Cell Struct. Funct. 23:315-323(1998).
 CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current
 CC when expressed in Xenopus oocytes. May be a modulator capable of
 CC activating endogenous oocyte channels.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the FXD family.
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AB015759; BA35078.1; -; mRNA.
 DR InterPro; IPR000272; FXD.
 DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
 DR PROSITE; PS01310; FXD; 1.
 KW Chloride; Chloride channel; Ion transport; Ionic channel; Signal;
 KW Transmembrane; Transport.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 88 FXD domain-containing ion transport
 FT regulator 3.
 FT TOPO_DOM 18 38 Extracellular (Potential).
 FT TRANSMEM 39 59 Potential.
 FT TOPO_DOM 60 88 Cytoplasmic (Potential).
 SQ SEQUENCE 88 AA; 9314 MW; 6CC7810B90512E5A CRC64;

Query Match 50.0%; Score 230.5; DB 1; Length 88;
 Best Local Similarity 57.8%; Pred. No. 1.1e-16;
 Matches 52; Conservative 10; Mismatches 25; Indels 3; Gaps 3;

RESULT 9
 ID FXD3_HUMAN STANDARD; PRT; 87 AA.
 AC Q14802; Q13211;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FXD domain-containing ion transport regulator 3 precursor (Chloride

DE conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein)
 GN (Phospholipid-1like).
 OS Name=FXVD3; Synonym=Mat8, PLML;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mammary gland;
 RX MEDLINE=95138184; PubMed=7836447; DOI=10.1074/jbc.270.15.8571;
 RA Morrison B.W., Moorman J.R., Kowaley G.C., Kobayashi Y.M., Jones L.R.,
 RA Leder P.,
 RA "Mat-8, a novel phospholipid-like protein expressed in human breast
 RA tumors, induces a chloride conductance in Xenopus oocytes.";
 RL J. Biol. Chem. 270:2176-2182 (1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung carcinoma;
 RA Lei W., Wu M.,
 RN Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=urinary bladder;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schin J.E., Jones S.J.W., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RA cDNA sequences.";
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current
 CC when expressed in Xenopus oocytes. May be a modulator capable of
 CC activating endogenous oocyte channels.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in a subset of human breast tumors.
 CC -1- MISCELLANEOUS: Marker of a cell type preferentially transformed by
 CC neu or ras oncoprotein.
 CC -1- SIMILARITY: Belongs to the FXVD family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, X93036; CAA63604.1; -, mRNA.
 CC EMBL, U28249; AAA73922.1; -, mRNA.
 CC EMBL, BC005238; AA05238.1; -, mRNA.
 CC PIR, A55571; A55571.
 CC Ensemble: ENSG00000089356; Homo sapiens.
 CC HGNC, HGNC:4027; FXVD3.
 CC H-InvDB, HIX0018290; -.
 CC MIM, 604996; -.
 CC GO, GO:0005887; C:integral to plasma membrane; TAS.
 CC GO, GO:0005254; P:chloride channel activity; TAS.
 CC GO, GO:0006821; P:chloride transport; TAS.
 CC InterPro, IPR000272; FXVD.

DR Pfam, PF02038; ATP1G1_PLM_Mat8; 1.
 DR PROSITE, PS01310; FXVD; 1.
 KW Chloride; Chloride channel; Ion transport; Ionic channel; Signal;
 KW Transmembrane; Transport.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 87 FXVD domain-containing ion transport
 FT TOPO_DOM 21 38 regulator 3.
 FT TRANSMEM 39 59 Extracellular (Potential).
 FT TOPO_DOM 60 87 Potential.
 FT CONFLICT 36 37 Cytoplasmic (Potential).
 FT CONFLICT 58 58 Missing (in Ref. 2).
 FT FT S-> SEMRSSGDEAGRGKSPPLTTQLSPNG (in Ref.
 FT FT 2).
 SQ SEQUENCE 87 AA; 9263 MW; 6D674D668EB32493 CRC64;
 Query Match 46.5%; Score 214.5; DB 1; Length 87;
 Best Local Similarity 54.5%; Pred. No. 5.6e-15;
 Matches 48; Conservative 11; Mismatches 24; Indels 5; Gaps 4;
 QY 1 MERVTLALL-LAGLTALNPANRDPYDKNLQLSGILAGIAYLGS 59
 DB 1 MOKVTGLVFLAGFVPLDAND-LDKNSPFYDMSLQVGGLICAGVLCAGIIVWSA 59
 QY 60 KCKTKSSOKO-HSPVPEKAIPLTPGSA 86
 DB 60 KCKCKFGQKSGH--PGETPLTPGSA 85
 RESULT 10
 ID Q61B59_HUMAN PRELIMINARY; PRT; 87 AA.
 AC Q61B59;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE FXVD3 protein (FXVD domain containing ion transport regulator 3,
 DE isoform 1).
 GN Name=FXVD3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Halleck A., Ebert L., Mkundinya M., Schick M., Eisenstein S.,
 RA Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., Labaer J.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
 RT vector.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=White Matter pool-5 brain tissues- femoral artery;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

[illegible]

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OC Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Liver.
RA Aoki T., Toyoda H., Nishimoto S., Tawara J., Komuraaki T.;
RT "Identification of VESP6, a vascular endothelial cell specific
RT protein.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RX MEDLINE=21105933; PubMed=11165383; DOI=10.1016/S0169-328X(00)00213-8;
RA Yamaguchi F., Yamaguchi K., Tai Y., Sugimoto K., Tokuda M.;
RT "Molecular cloning and characterization of a novel phospholipase-like
RT protein from rat hippocampus.";
RL Brain Res. Mol. Brain Res. 86:189-192(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 1).
RC TISSUE=Lung;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=G91XV6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=G91XV6-2; Sequence=VSP_001586;
CC -1- SIMILARITY: Belongs to the FYXD family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB030908; BAB62242.1; -; mRNA.
DR EMBL; AF142439; AAF66613.1; -; mRNA.
DR EMBL; BC072528; AAH72528.1; -; mRNA.
DR Ensemble; ENSRNOG0000016412; Rattus norvegicus.
DR RGD; 69315; Fxyd6.
DR InterPro; IPR000272; FYXD.
DR Pfam; PF02038; ATP1G1_PLM_MAT9; 1.
DR PROSITE; PS01310; FXYD; 1.
KW Alternative splicing; Ion transport; Ionic channel; Signal;
KW Transmembrane; Transport.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 94 FYXD domain-containing ion transport
FT FT regulator 6.
FT TOPO_DOM 18 34 Extracellular (Potential).
FT TRANSMEM 35 57 Potential.
FT TOPO_DOM 58 94 Cytoplasmic (Potential).
FT FT Missing (in isoform 2).
FT VARSPLC 20 20 /Ftrd=VSP_001586.
FT FT N -> S (in Ref. 2).
FT FT CONFLICT 65 65 NCD035FAC0572451 CRC64;
SQ SEQUENCE 94 Aa, 10388 Mw, 1CDD35FAC0572451 CRC64;

Query Match 27.0%; Score 124.5; DB 1; Length 94;
Best Local Similarity 37.5%; Pred. No. 2,46-05;
Matches 33; Conservative 15; Mismatches 37; Indels 3; Gaps 2;

QY 1 MERTALLALLAGTLEANDPFRANKDPPFYDMKNQLSGLTGCGGLATAGIAVLSGK 60
DB 1 MERVLLICSLAPVVLASAEKEKEK-DPEFYDYQTLIGLTVAVVLFVSGVILLISRR 59
QY 61 CKYSSQKQSPVPEKA--IPLIRGSA 86
DB 60 CKCSFNQKPRAPGDEBAQVENTLITNNA 87

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Job time : 234 secs
